

# SCORE Search Results Details for Application 09556178 and Search Result 20101203\_114247\_us-09-556-178-1.rag.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203\_114247\_us-09-556-178-1.rag.

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GenCore version 6.3  
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:51 ; Search time 74 Seconds  
(without alignments)  
9429.236 Million cell updates/sec

Title: US-09-556-178-1  
Perfect score: 2898  
Sequence: 1 MNVVFVAVKQYISKMIEDSGP.....GLHSRSKESSQVTSRSASRR 570

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6395994 seqs, 1224146475 residues

Total number of hits satisfying chosen parameters: 6395994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_201023:\*  
1: geneseq1:\*  
2: geneseq2:\*  
3: geneseq3:\*

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2898	100.0	570	1	AAY49958	Aay49958 Human ves
2	2898	100.0	570	1	AAB03813	Aab03813 Human ves
3	2898	100.0	570	1	AAB94478	Aab94478 Human pro
4	2898	100.0	570	1	ADE61224	Ade61224 Human Pro
5	2898	100.0	570	1	ADP12603	Adp12603 Protein e
6	2898	100.0	570	1	ADR99181	Adr99181 Vacuolar
7	2898	100.0	570	2	AJF47297	Ajf47297 Human MCR
8	2898	100.0	570	3	AYE14424	Aye14424 Allograft
9	2844	98.1	570	1	ABB57217	Abb57217 Mouse isc
10	2840	98.0	570	1	ADE61222	Ade61222 Rat Prote
11	2815.5	97.2	578	1	ABG04478	Abg04478 Novel hum
12	1920	66.3	390	1	AAO21766	Aao21766 Human rib
13	1584	54.7	574	1	ABB63752	Abb63752 Drosophil
14	1584	54.7	574	2	AFB98005	Afb98005 Fruit fly

15	1310	45.2	441	1	ABG04479	Abg04479	Novel hum
16	1299.5	44.8	567	2	AQD50046	Aqd50046	Rice cDNA
17	1286	44.4	568	2	ANL98635	Anl98635	Oryza sat
18	1270	43.8	567	3	AWV44951	Aww44951	Plant pro
19	1026.5	35.4	210	1	AA07020	Aay07020	Breast ca
20	976	33.7	577	1	ABR53033	Abr53033	Protein s
21	976	33.7	577	1	ADK62860	Adk62860	Disease t
22	949.5	32.8	472	3	AXH20971	Axh20971	Zea mays
23	786.5	27.1	329	3	AWP61628	Awp61628	Aspergill
24	778.5	26.9	722	1	AAB18291	Aab18291	Plasmodiu
25	753	26.0	364	2	AQD41760	Aqd41760	Rice cDNA
26	714	24.6	165	1	AA004331	Aao04331	Human pol
27	574	19.8	219	2	ARO38966	Aro38966	Soybean c
28	574	19.8	219	3	AXJ12112	Axj12112	Heteroder
29	510.5	17.6	184	2	ARO77042	Aro77042	Soybean c
30	510.5	17.6	184	3	AXJ50188	Axj50188	Heteroder
31	492	17.0	230	1	AFR53396	Afr53396	Recombina
32	492	17.0	230	3	AXD18698	Axd18698	Sorghum b
33	469.5	16.2	186	2	ARO80389	Aro80389	Soybean c
34	469.5	16.2	186	3	AXJ53535	Axj53535	Heteroder
35	416	14.4	212	3	AWP61629	Awp61629	Aspergill
36	407	14.0	621	2	ARM75723	Arm75723	Arabidops
37	407	14.0	633	1	AAG50809	Aag50809	Arabidops
38	407	14.0	633	2	ALJ97173	Alj97173	Plant pro
39	407	14.0	653	2	ARM75722	Arm75722	Arabidops
40	407	14.0	662	1	AAG50808	Aag50808	Arabidops
41	407	14.0	662	2	ALJ97172	Alj97172	Plant pro
42	401	13.8	633	1	AAG18696	Aag18696	Arabidops
43	401	13.8	633	2	ALJ52955	Alj52955	Plant pro
44	401	13.8	633	2	ARM38817	Arm38817	Arabidops
45	401	13.8	662	1	AAG18695	Aag18695	Arabidops

## ALIGNMENTS

## RESULT 1

AAY49958

ID AAY49958 standard; protein; 570 AA.

XX

AC AAY49958;

XX

DT 15-JUN-2007 (revised)

DT 04-FEB-2000 (first entry)

XX

DE Human vesicle trafficking protein 1.

XX

KW Human; vesicle trafficking protein; VTP-1; VTP-2; VTP-3; apoptosis;

KW cancer; inflammation; BOND\_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;

KW G05798; G06886; G06904; G06954; G016020; G016192.

XX

OS Homo sapiens.

XX

PN US5989859-A.  
 XX  
 PD 23-NOV-1999.  
 XX  
 PF 07-NOV-1997; 97US-00967364.  
 XX  
 PR 07-NOV-1997; 97US-00967364.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Bandman O, Guegler KJ, Corley NC, Lal P, Shah P;  
 XX  
 DR WPI; 2000-022782/02.  
 DR N-PSDB; AAZ35833.  
 DR PC:NCBI; gi18105063.  
 DR PC:SWISSPROT; Q9NRW7.  
 DR PC:BIND; 261868, 261869.  
 XX  
 PT Novel vesicle trafficking proteins used in the diagnosis, prevention, and  
 PT treatment of inflammation or cancer.  
 XX  
 PS Claim 9; Fig 1; 55pp; English.  
 XX  
 CC The present sequence represents the human vesicle trafficking protein  
 CC designated VTP-1. VTPs can be used in a method for preventing or treating  
 CC disease associated with an increase in apoptosis. The method can treat  
 CC diseases such as cancer and inflammation, by administering a VTP  
 CC antagonist  
 CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.  
 XX  
 SQ Sequence 570 AA;

	Query Match	100.0%;	Score 2898;	DB 1;	Length 570;				
	Best Local Similarity	100.0%;							
	Matches	570;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps 0;
Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60						
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60						
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120						
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120						
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180						
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180						
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240						
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240						
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300						
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300						
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRLVSEARNLLEVSEVEQELACQ	360						
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRLVSEARNLLEVSEVEQELACQ	360						
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420						
Db	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420						
Qy	421	KLVSAVVEYGGKRVGRSDFLSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETLDHLIKG	480						

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Db      421  KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
      |||
Qy      481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
      |||
Db      481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
      |||
Qy      541  KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
      |||
Db      541  KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

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## RESULT 2

AAB03813

ID AAB03813 standard; protein; 570 AA.

XX

AC AAB03813;

XX

DT 15-JUN-2007 (revised)

DT 13-OCT-2000 (first entry)

XX

DE Human vesicle trafficking protein-1 (VTP-1) amino acid sequence.

XX

KW Vesicle trafficking protein; VTP-1; human; cancer; inflammation; asthma;

KW foetal development; Crohn's disease; diabetes; multiple sclerosis;

KW rheumatoid arthritis; infection; ulcerative colitis; proliferation;

KW irritable bowel syndrome; apoptosis; AIDS; Alzheimer's disease;

KW Parkinson's disease; osteoporosis; wasting disorder; BOND\_PC;

KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;

KW G05798; G06886; G06904; G06954; G016020; G016192.

XX

OS Homo sapiens.

XX

PN US6071703-A.

XX

PD 06-JUN-2000.

XX

KF 04-AUG-1999; 99US-00368408.

XX

PR 07-NOV-1997; 97US-00967364.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Guegler KJ, Shah P, Corley NC, Bandman O, Lal P;

XX

DR WPI; 2000-422079/36.

DR N-PSDB; AAA59873.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Identifying polynucleotides encoding vesicle trafficking proteins (VTP)

PT for treating and preventing e.g. inflammation, by detecting a

PT hybridization complex of a nucleic acid from a sample and a

PT polynucleotide encoding a VTP.  
 XX  
 PS Example; Fig 1; 55pp; English.  
 XX  
 CC This sequence represents human vesicle trafficking protein (VTP-1) amino  
 CC acid sequence. VTP-1 encoding cDNA was isolated from a THP-1 cell line  
 CC cDNA library (THP1PEB01). VTP-1 has structural and chemical homology with  
 CC a mouse vacuolar protein-sorting protein mVps45. The present invention  
 CC relates to a method for detecting human VTP encoding polynucleotide  
 CC sequences and includes nucleotide and protein sequences for human VTP-1,  
 CC VTP-2 and VTP-3. Northern analysis of VTP-1, 2, and 3 shows that their  
 CC expression is associated with cancer, inflammation and foetal/infant  
 CC development. The method of the invention is useful for screening and  
 CC identifying a polynucleotide encoding a human VTP, which may be used for  
 CC the diagnosis, prevention, or treatment of inflammation associated  
 CC disorder, e.g. asthma, Crohn's disease, diabetes, multiple sclerosis,  
 CC rheumatoid arthritis, infections, ulcerative colitis and irritable bowel  
 CC syndrome. Other diseases and disorders identified, prevented or treated  
 CC with polynucleotide sequences encoding VTP include those associated with  
 CC cell proliferation or apoptosis, such as AIDS, Alzheimer's disease,  
 CC Parkinson's disease, osteoporosis, wasting diseases and cancer  
 CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.  
 XX  
 SQ Sequence 570 AA;

Query Match		100.0%;	Score 2898;	DB 1;	Length 570;		
Best Local Similarity		100.0%;					
Matches	570;	Conservative	0;	Mismatches	0;	Indels	0;
		Gaps	0;				
Qy	1	MNVVFAVKQYISKMIEDSGPMKVL	MDKET	TGIVSMVYTQSEILQKEVYLFERIDSQNR	60		
Db	1	MNVVFAVKQYISKMIEDSGPMKVL	MDKET	TGIVSMVYTQSEILQKEVYLFERIDSQNR	60		
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS	LAEAEQEVEVA	120			
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS	LAEAEQEVEVA	120			
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180				
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180				
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240				
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240				
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300				
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300				
Qy	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSE RNLLLEVSEVEQELACQ	360				
Db	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSE RNLLLEVSEVEQELACQ	360				
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMMDLRNKGVSEKYR	420				
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMMDLRNKGVSEKYR	420				
Qy	421	KLVS AVVEYGGKRRVSGDLSFKPDVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIKG	480				
Db	421	KLVS AVVEYGGKRRVSGDLSFKPDVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIKG	480				
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540				
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540				

Qy 541 KSFLEEVLASGLHSRSKESQVTSRSASRR 570  
 ||||||||||||||||||||||||||||||||  
 Db 541 KSFLEEVLASGLHSRSKESQVTSRSASRR 570

# RESULT 3

AAB94478

ID AAB94478 standard; protein; 570 AA.

XX

AC AAB94478;

XX

DT 15-JUN-2007 (revised)

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:15151.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy;

KW BOND\_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;

KW G05798; G06886; G06904; G06954; G016020; G016192.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC FOR BIOTECHNOLOGY.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

DR PC:NCBI; g118105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-

PT length cDNAs defined in the specification, and for the detection and/or

PT diagnosis of the abnormality of the proteins encoded by the full-length

PT cDNAs.

XX

PS Claim 8; SEQ ID NO 15151; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-

length cDNAs defined in the specification. Where a primer set comprises:  
(a) an oligo-dT primer and an oligonucleotide complementary to the  
complementary strand of a polynucleotide which comprises one of the 5602  
nucleotide sequences defined in the specification, where the  
oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
of an oligonucleotide comprising a sequence complementary to the  
complementary strand of a polynucleotide which comprises a 5'-end  
sequence and an oligonucleotide comprising a sequence complementary to a  
polynucleotide which comprises a 3'-end sequence, where the  
oligonucleotide comprises at least 15 nucleotides and the combination of  
the 5'-end sequence/3'-end sequence is selected from those defined in the  
specification. The primer sets can be used in antisense therapy and in  
gene therapy. The primers are useful for synthesising polynucleotides,  
particularly full-length cDNAs. The primers are also useful for the  
detection and/or diagnosis of the abnormality of the proteins encoded by  
the full-length cDNAs. The primers allow obtaining of the full-length  
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893  
represent human amino acid sequences; and AAH13629 to AAH13632 represent  
oligonucleotides, all of which are used in the exemplification of the  
present invention

Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
information from BOND.

XX  
SQ Sequence 570 AA;

	Query Match	100.0%;	Score 2898;	DB 1;	Length 570;
	Best Local Similarity	100.0%;			
	Matches 570;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60			
Db	1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60			
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEQEVEVA	120			
Db	61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEQEVEVA	120			
Qy	121 EVQEFYGDYIAVNPFLFSLNLGCGQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180			
Db	121 EVQEFYGDYIAVNPFLFSLNLGCGQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180			
Qy	181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWITYQAMVHELL	240			
Db	181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWITYQAMVHELL	240			
Qy	241 GINNNRIDLRSVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNINKNLMEDFQKKPKP	300			
Db	241 GINNNRIDLRSVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNINKNLMEDFQKKPKP	300			
Qy	301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRVLSERNLLEVSEVEQELACQ	360			
Db	301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRVLSERNLLEVSEVEQELACQ	360			
Qy	361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR	420			
Db	361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR	420			
Qy	421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIK	480			
Db	421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIK	480			
Qy	481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540			
Db	481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540			

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570  
 ||||||||||||||||||||||||||||||||  
 Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

## RESULT 4

ADE61224

ID ADE61224 standard; protein; 570 AA.

XX

AC ADE61224;

XX

DT 15-JUN-2007 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Human Protein NP\_009189, SEQ ID NO 7142.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung; BOND\_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;

KW G05798; G06886; G06904; G06954; G016020; G016192.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; NP\_009189.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell



comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Revised record issued on 15-JUN-2007 : Enhanced with precomputed information from BOND.

Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;  
Best Local Similarity 100.0%;  
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEQEYVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEQEYVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540

Db 481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTYVNLNRTTPGVRIVLGGTTVHNT 540

QY 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570  
 |||

Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

# RESULT 5

ADP12603

ID ADP12603 standard; protein; 570 AA.

XX

AC ADP12603;

XX

DT 15-JUN-2007 (revised)

DT 12-AUG-2004 (first entry)

XX

DE Protein encoded by mRNA of the invention #213.

XX

KW transplant rejection; immune system; rheumatoid arthritis; lupus;

KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; BOND\_PC;

KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA\_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;

G05798; G06886; G06904; G06954; G016020; G016192.

XX

OS Homo sapiens.

XX

PN WO2004042346-A2.

XX

PD 21-MAY-2004.

XX

PF 24-APR-2003; 2003WO-US012946.

XX

PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX

PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

Rosenberg S;

XX

DR WPI; 2004-400724/37.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,

PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant

PT rejection, in an individual, comprises detecting the expression level of

PT the genes.

XX

PS Claim 65; SEQ ID NO 2612; 1762pp; English.

XX

CC The present invention relates to diagnosing or monitoring transplant

CC rejection, e.g. cardiac or kidney transplant rejection, in an individual

CC comprises detecting the expression level of one or more genes. The

CC methods, system and kits are useful in diagnosing or monitoring  
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic  
 CC islet, lung, bone marrow or stem cell transplant rejection,  
 CC xenotransplant rejection or mechanical organ replacement rejection, in an  
 CC individual. The method is also useful in assessing the immune status of  
 CC an individual. The methods are also useful in diagnosing and monitoring  
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,  
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or  
 CC viral, bacterial or fungal infection. The present sequence represents a  
 CC protein that is encoded by the mRNA of the invention.

CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.

XX  
 SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;  
 Best Local Similarity 100.0%;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKPKP	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKPKP	300
Qy	301	EQQKLESIA DMKAFVENY PQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENY PQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPF L HETL D H L I K G	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPF L HETL D H L I K G	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEV LASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEV LASGLHSRSKESQVTSRSASRR	570

RESULT 6

ADR99181

ID ADR99181 standard; protein; 570 AA.

XX

AC ADR99181;

XX

DT 15-JUN-2007 (revised)  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Vacuolar protein sorting 45A, VSP45A, SEQ ID 187.  
 XX  
 KW Cytostatic; breast cancer; cancer; human; Vacuolar protein sorting 45A;  
 KW VSP45A; BOND\_PC; vacuolar protein sorting 45A;  
 KW leucocyte vacuolar protein sorting 45;  
 KW vacuolar protein sorting 45B (yeast);  
 KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;  
 KW VPS45B; VPS54A; VSP45A; H1VPS45;  
 KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;  
 KW vacuolar protein sorting 45A (yeast), isoform CRA\_a;  
 KW vacuolar protein sorting 45A (yeast), isoform CRA\_a [Homo sapiens];  
 KW vacuolar protein sorting 45A (yeast);  
 KW vacuolar protein sorting 45A (yeast) [Homo sapiens];  
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);  
 KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];  
 KW vacuolar protein sorting 45 isoform;  
 KW vacuolar protein sorting 45 isoform [Homo sapiens];  
 KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;  
 KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004078035-A2.  
 XX  
 PD 16-SEP-2004.  
 XX  
 PF 27-FEB-2004; 2004WO-US007268.  
 XX  
 PR 28-FEB-2003; 2003US-0450655P.  
 XX  
 PA (FARB ) BAYER PHARM CORP.  
 XX  
 PI Eveleigh D, Bigwood D;  
 XX  
 DR WPI; 2004-653556/63.  
 DR N-PSDB; ADR99054.  
 DR PC:NCBI; gi18105063.  
 DR PC:SWISSPROT; Q9NRW7.  
 DR PC:BNID; 261868, 261869.  
 XX  
 PT Diagnosing breast cancer comprises comparing the level of expression of  
 PT genes or gene products in a first biological sample taken from a patient  
 PT with that in a normal patient sample.  
 XX  
 PS Claim 3; SEQ ID NO 187; 53pp; English.  
 XX  
 CC The present invention relates to a method (M1) for diagnosing breast  
 CC cancer in a patient. The method comprises comparing the level of  
 CC expression of one or more genes or gene products in a biological sample  
 CC from the patient with that in a normal patient sample, where a difference  
 CC in the gene expression in the first sample compared to that in the second  
 CC sample is a diagnostic of the disease. Also claimed are: method (M2) for  
 CC distinguishing between normal and disease tissues; method (M3) for  
 CC monitoring the response of a breast cancer patient to treatment with an  
 CC anti-cancer agent; method (M4) for identifying a compound for treating  
 CC breast cancer; and an array for distinguishing between normal and disease  
 CC tissues comprising two or more probes corresponding to genes selected  
 CC from ADR98995-ADR99121 or comprising two or more polypeptides selected  
 CC from ADR99122-ADR99248. In M1 and M2 the genes are selected from ADR98995  
 CC -ADR99121 and the gene products are polypeptides selected from ADR99122-  
 CC ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are  
 CC useful for distinguishing between normal and disease tissue. M3 is useful  
 CC for monitoring the response of a breast cancer patient to treatment with  
 CC an anti-cancer agent. M4 is useful for identifying a compound for

CC treating breast cancer. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.  
 XX  
 SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;  
 Best Local Similarity 100.0%;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYIFYFSNVISKSDVKS LAEAEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYIFYFSNVISKSDVKS LAEAEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKPKP	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKPKP	300
Qy	301	EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGKRVIRLVGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGKRVIRLVGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

## RESULT 7

AJF47297

ID AJF47297 standard; protein; 570 AA.

XX

AC AJF47297;

XX

DT 01-NOV-2007 (first entry)

XX

DE Human MCR vacuolar protein sorting 45A (VPS45A).

XX

KW Diagnosis; prognosis; prophylaxis; therapeutic; drug screening;

KW diagnostic; transgenic animal; pharmacogenetics; cancer;

KW multiple myeloma; cytostatic; melanoma; breast tumor; lung tumor;

KW colorectal tumor; prostate tumor; pancreas tumor; stomach tumor;  
 KW ovary tumor; bladder tumor; brain tumor; central nervous system tumor;  
 KW esophagus tumor; uterine cervix tumor; uterus tumor;  
 KW endometroid carcinoma; mouth tumor; pharynx tumor; liver tumor;  
 KW renal tumor; testis tumor; biliary tumor; thyroid tumor; adrenal tumor;  
 KW osteosarcoma; chondrosarcoma; hematological tumor; macroglobulinemia;  
 KW gammopathy; amyloidosis; tumor marker; BOND\_PC;  
 KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;  
 KW vacuolar protein sorting 45B (yeast); VPS45A; H1; VPS45; VSP45; VPS45B;  
 KW VPS54A; VSP45A; H1VPS45; vacuolar protein sorting 45A (yeast homolog);  
 KW VPS54A, VPS45B; vacuolar protein sorting 45A (yeast), isoform CRA\_a;  
 KW vacuolar protein sorting 45A (yeast);  
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);  
 KW vacuolar protein sorting 45 isoform; unnamed protein product; GO5764;  
 KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2007095186-A2.  
 XX  
 PD 23-AUG-2007.  
 XX  
 PF 13-FEB-2007; 2007WO-US003697.  
 XX  
 PR 14-FEB-2006; 2006US-0773072P.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX  
 PI Depinho RA;  
 XX  
 DR WPI; 2007-701669/65.  
 DR N-PSDB; AJF46910.  
 DR REFSEQ; NP\_009190.  
 DR PC:NCBI; gi18105063.  
 DR PC:SWISSPROT; Q9NRW7.  
 DR PC:BIND; 261868, 261869.  
 XX  
 PT Assessing whether a subject is afflicted with cancer for treating or  
 PT preventing cancer comprises determining an altered copy number of a  
 PT minimal common region (MCR) in a subject sample compared to a normal copy  
 PT number of the MCR.  
 XX  
 PS Disclosure; Page; 158pp; English.  
 XX  
 CC The present invention provides a method for assessing whether a subject  
 CC is afflicted with cancer or at risk for developing cancer. The method  
 CC involves comparing the copy number of a minimal common region (MCR) in a  
 CC subject sample to the normal copy number of the MCR, where an altered  
 CC copy number of the MCR in the sample and/or alterations in the amount,  
 CC structure and/or activity of one or more of the markers (PRKC15, SEMA4A,  
 CC DHH36, GPR86 and combinations thereof) indicates that the subject is  
 CC afflicted with cancer or at risk for developing cancer. The invention is  
 CC useful for the diagnosis, prognosis, prevention and treatment of cancers  
 CC such as B cell cancer, multiple melanoma, myleoma, breast cancer, lung  
 CC cancer, bronchus cancer, colorectal cancer, prostate cancer, pancreatic  
 CC cancer, stomach cancer, ovarian cancer, urinary bladder cancer, brain or  
 CC central nervous system cancer, peripheral nervous system cancer,  
 CC esophageal cancer, cervical cancer, uterine or endometrial cancer, cancer  
 CC of the oral cavity or pharynx, liver cancer, kidney cancer, testicular  
 CC cancer, biliary tract cancer, small bowel or appendix cancer, salivary  
 CC gland cancer, thyroid gland cancer, adrenal gland cancer, osteosarcoma,  
 CC chondrosarcoma and cancer of hematological tissues and also Waldenstrom's  
 CC macroglobulinemia, heavy chain diseases (alpha chain disease, gamma chain  
 CC disease, mu chain disease, benign monoclonal gammopathy and immunocytic  
 CC amyloidosis). The invention is also useful in diagnostic assays,  
 CC pharmacogenomics, drug screening and in the production of transgenic  
 CC animals. The present sequence is a human minimal common region (MCR)

CC protein. Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed  
 CC information from BOND.  
 XX  
 SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 2; Length 570;  
 Best Local Similarity 100.0%;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKPK	300
Qy	301	EQQKLESIA DMKAFVENYYPQFKKMSGTVSKHVTVGELSRVSE RNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENYYPQFKKMSGTVSKHVTVGELSRVSE RNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

## RESULT 8

AYE14424

ID AYE14424 standard; protein; 570 AA.

XX

AC AYE14424;

XX

DT 02-SEP-2010 (first entry)

XX

DE Allograft rejection diagnosis/prognosis marker protein, SEQ:2612.

XX

KW diagnostic test; gene expression; heart transplant rejection;

KW immunosuppressive; prognosis; rna quantitation; transplant rejection;

KW BOND\_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;  
KW vacuolar protein sorting 45B (yeast); VPS45A; H1; VPS45; VSP45; VPS45B;  
KW VPS54A; VSP45A; H1VPS45; vacuolar protein sorting 45A (yeast homolog);  
KW VPS54A, VPS45B; vacuolar protein sorting 45A (yeast), isoform CRA\_a;  
KW vacuolar protein sorting 45A (yeast);  
KW vacuolar protein sorting 45 homolog (S. cerevisiae);  
KW vacuolar protein sorting 45 isoform; unnamed protein product; GO5764;  
KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2010151467-A1.  
XX  
PD 17-JUN-2010.  
XX  
PF 08-SEP-2009; 2009US-00584615.  
XX  
PR 24-APR-2003; 2003WO-US012946.  
PR 22-JUL-2005; 2005US-00511937.  
XX  
PA (XDDX-) XDX INC.  
XX  
PI Fry K, Ly N, Morris M, Prentice J, Rosenberg S, Wohlgenuth J;  
PI Woodward R;  
XX  
DR WPI; 2010-G86279/41.  
DR PC:NCBI; gi18105063.  
DR PC:SWISSPROT; Q9NRW7.  
DR PC:BIND; 261868, 261869.  
XX  
PT Diagnosing or monitoring transplant rejection comprises detecting the  
PT expression level of a nucleic acid in the patient to diagnose or monitor  
PT transplant rejection in the patient.  
XX  
PS Example 1; SEQ ID NO 2612; 146pp; English.  
XX  
CC The present invention relates to a method for diagnosing or monitoring  
CC transplant rejection, particularly cardiac transplant rejection in a  
CC patient. The method comprises detecting the expression level of a gene  
CC sequence preferably AYE11908 in a patient, by measuring the RNA level  
CC expressed by the gene sequence. AYE14212-AYE14438 are proteins encoded by  
CC gene expression markers AYE12145-AYE12476 for diagnosing and monitoring  
CC allograft rejection.  
CC  
CC Revised record issued on 19-AUG-2010 : Enhanced with precomputed  
CC information from BOND.  
XX  
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 3; Length 570;  
Best Local Similarity 100.0%;  
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFRERIDSNQR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFRERIDSNQR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWYQAMVHELL	240



```

Db      181 SEAAKRLAECVKQVITKEYELFEFRRTVPPLLLILDRCDDAITPLLNQWTVQAMVHELL 240
Qy      241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
      |||
Db      241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
Qy      301 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
      |||
Db      301 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Qy      361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR 420
      |||
Db      361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR 420
Qy      421 KLVSAVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYVYTHQPFLLHETDLHLIKG 480
      |||
Db      421 KLVSAVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYVYTHQPFLLHETDLHLIKG 480
Qy      481 RLKENLYPYLPGSTLDRPDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
      |||
Db      481 RLKENLYPYLPGSTLDRPDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Qy      541 KSFLFEEVLASGLHSRSKESSQVTSRSASRR 570
      |||
Db      541 KSFLFEEVLASGLHSRSKESSQVTSRSASRR 570

```

RESULT 9

ABB57217

```

ID      ABB57217 standard; protein; 570 AA.
XX
AC      ABB57217;
XX
DT      15-JUN-2007 (revised)
DT      07-MAR-2002 (first entry)
XX
DE      Mouse ischaemic condition related protein sequence SEQ ID NO:527.
XX
KW      Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW      vasospastic ischaemia; ischaemic condition; ischaemic disease; BOND_PC;
KW      vacuolar protein sorting 45;
KW      vacuolar protein sorting-associated protein 45;
KW      vacuolar protein sorting protein 45;
KW      vacuolar protein sorting 45 [Mus musculus]; Vps45; mVps45; AI462172;
KW      AW554165; vacuolar protein sorting 45 (yeast);
KW      Vacuolar protein sorting 45 (yeast) [Mus musculus];
KW      vacuolar protein sorting homolog;
KW      vacuolar protein sorting homolog [Mus musculus]; GO5515; GO6810; GO6904;
KW      GO15031; GO16020; GO16192.
XX
OS      Mus musculus.
XX
PN      WO200188188-A2.
XX
PD      22-NOV-2001.
XX
PF      18-MAY-2001; 2001WO-JP004192.
XX
PR      18-MAY-2000; 2000JP-00145977.
XX
PA      (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI      Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR      WPI; 2002-034733/04.
DR      N-PSDB; ABI99530.
DR      PC:NCBI; gi7305631.

```

DR PC:SWISSPROT; P97390.  
 DR PC:BIND; 261867.  
 XX  
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or by  
 PT determining the expression profile of a gene group comprising these  
 PT genes.  
 XX  
 PS Claim 2; Page 1446-1448; 2690pp; English.  
 XX  
 CC The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the  
 CC protein sequences in ABB57020 to ABB57374) or by determining the  
 CC expression profile of a gene group comprising these genes. The expression  
 CC levels or expression profiles produced by these genes are used as an  
 CC indicator when screening for ischaemic condition-improving drugs or  
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR  
 CC primers for a mouse ischaemic condition related sequence, which are used  
 CC in the exemplification of the present invention  
 CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.  
 XX  
 SQ Sequence 570 AA;

Query Match 98.1%; Score 2844; DB 1; Length 570;  
 Best Local Similarity 97.0%;  
 Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEYVVA	120
Db	61	EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEYVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCCDAITPLLNQWYTYQAMVHELL	240
Db	181	SEAAKRLGECVKQVISKEYELFEFRRTVEVPLLLILDRCCDAITPLLNQWYTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKPKP	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKRPK	300
Qy	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVSE RNLLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVSE RNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR	420
Db	361	NDHSSALQNVKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLIVDLRSKGVAEKYR	420
Qy	421	KLVS AVVEYGGKRV RGSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRV RGSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLP GSTLRDRPQDIIVFVIGGATYEEALTVYNLRNTPGVRIVLGGETTVHNT	540

```

Db      481  |||||||||||||||||||||:|||||||||||||||||||||:||||
Qy      541  KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
Db      541  |||||||||||||||||||:|||| |||||:||
Db      541  KSFLEEVLASGLHSRSRESSQATSRSANRR 570

```

## RESULT 10

ADE61222

ID ADE61222 standard; protein; 570 AA.

XX

AC ADE61222;

XX

DT 15-JUN-2007 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein AAB53041, SEQ ID NO 7140.

XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung;

KW BOND\_PC; vacuolar protein sorting 45; vesicular transport protein rvps45;

KW vacuolar protein sorting 45 [Rattus norvegicus]; Vps45; Vsp45a; MGC;

KW MGC93104; vacuolar protein sorting 45 (yeast);

KW Vacuolar protein sorting 45 (yeast) [Rattus norvegicus]; rvps45;

KW rvps45 [Rattus norvegicus]; G05515; G05764; G05798; G06886; G06904;

KW G06954; G015031; G016020; G016192.

XX

OS Rattus norvegicus.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; AAB53041.

DR PC:NCBI; gi25742604.

DR PC:SWISSPROT; O08700.

XX

PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.

XX  
 SQ Sequence 570 AA;

Query Match 98.0%; Score 2840; DB 1; Length 570;  
 Best Local Similarity 97.2%;  
 Matches 554; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDSLIIQELRRPKYTIYFIYFISNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLGECVKQVISKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKRPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKRPK	300
Qy	301	EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGSEKYR	420
Db	361	NDHSSALQNVKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGIVDLRSKGVAEKYR	420
Qy	421	KLVSAAVVEYGGKRVSGDLSFKPDVAITKQFLKLGKGVENVYTOHPFLHETLDHLIKG	480
Db	421	KLVSAAVVEYGGKRVSGDLSFKPDVAITKQFLKLGKGVENVYTOHPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	KLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTIHNT	540
Qy	541	KSFLEEVLASGLHSRSKSSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSRESSQATRSASRR	570

RESULT 11

ABG04478  
 ID ABG04478 standard; protein; 578 AA.  
 XX  
 AC ABG04478;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #4469.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR N-PSDB; AAS68665.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 20; SEQ ID NO 34837; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 578 AA;

Query Match 97.2%; Score 2815.5; DB 1; Length 578;  
 Best Local Similarity 97.7%;  
 Matches 558; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60  
 |||

http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780f9eb64&ItemName=2010... 1/10/1

# SCORE Search Results Details for Application 09556178 and Search Result 20101203\_114247\_us-09-556-178-1.rup.

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GenCore version 6.3  
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 347 Seconds  
(without alignments)  
6830.570 Million cell updates/sec

Title: US-09-556-178-1  
Perfect score: 2898  
Sequence: 1 MNVVFVAVKQYISKMIEDSGP.....GLHSRSKSSQVTSRSASRR 570

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 12869322 seqs, 4158259533 residues

Total number of hits satisfying chosen parameters: 12869322

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_201011:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*  
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2898	100.0	570	1	VPS45_HUMAN	Q9nrw7 RecName: Fu
2	2898	100.0	570	2	D3DUZ9_HUMAN	D3duz9 SubName: Fu
3	2888	99.7	570	2	Q53FR8_HUMAN	Q53fr8 SubName: Fu
4	2868	99.0	570	2	D2HBV3_AILME	D2hvb3 SubName: Fu
5	2864	98.8	570	2	A4FUX9_BOVIN	A4fux9 SubName: Fu
6	2844	98.1	570	1	VPS45_MOUSE	P97390 RecName: Fu
7	2841	98.0	570	2	Q3THX4_MOUSE	Q3thx4 SubName: Fu
8	2840	98.0	570	1	VPS45_RAT	O08700 RecName: Fu
9	2716	93.7	534	2	B7Z360_HUMAN	B7z360 SubName: Fu
10	2561	88.4	570	2	Q0D2D9_XENTR	Q0d2d9 SubName: Fu
11	2552	88.1	570	2	Q5XHB0_XENLA	Q5xhb0 SubName: Fu
12	2426	83.7	568	2	A8E7N5_DANRE	A8e7n5 SubName: Fu
13	2308	79.6	543	2	Q4TAW3_TETNG	Q4taw3 SubName: Fu
14	2244	77.4	445	2	B7Z5E4_HUMAN	B7z5e4 SubName: Fu
15	2164.5	74.7	538	2	B7Z5D4_HUMAN	B7z5d4 SubName: Fu
16	2129.5	73.5	571	2	C3Y1S4_BRAFL	C3yls4 SubName: Fu
17	2128.5	73.4	434	2	B7Z1J7_HUMAN	B7z1j7 SubName: Fu
18	1971	68.0	568	2	A7S9U5_NEMVE	A7s9u5 SubName: Fu

19	1920	66.3	390	2	A0AR27_HUMAN	A0ar27 SubName: Fu
20	1764	60.9	377	2	Q5ZJG4_CHICK	Q5zjg4 SubName: Fu
21	1711.5	59.1	548	2	B3RRU0_TRIAD	B3rru0 SubName: Fu
22	1693.5	58.4	569	2	D7EHQ8_TRICA	D7ehq8 SubName: Fu
23	1587.5	54.8	574	2	B3NZQ1_DROER	B3nzq1 SubName: Fu
24	1584	54.7	574	2	B4PUQ8_DROYA	B4puq8 SubName: Fu
25	1584	54.7	574	2	Q9VHB5_DROME	Q9vhb5 SubName: Fu
26	1583	54.6	388	2	B5X429_SALSA	B5x429 SubName: Fu
27	1578.5	54.5	564	2	B4QWK4_DROSI	B4qwk4 SubName: Fu
28	1577.5	54.4	574	2	B4JFE0_DROGR	B4jfe0 SubName: Fu
29	1576.5	54.4	574	2	B4M4B7_DROVI	B4m4b7 SubName: Fu
30	1574	54.3	574	2	B3M2G2_DROAN	B3m2g2 SubName: Fu
31	1569	54.1	574	2	Q295J1_DROPS	Q295j1 SubName: Fu
32	1562	53.9	574	2	B4NB39_DROWI	B4nb39 SubName: Fu
33	1560	53.8	575	2	D3TNU1_GLOMM	D3tnu1 SubName: Fu
34	1556.5	53.7	574	2	B4K664_DROMO	B4k664 SubName: Fu
35	1547.5	53.4	316	2	Q5T4Q0_HUMAN	Q5t4q0 SubName: Fu
36	1533	52.9	601	2	E0VVD5_PEDHC	E0vvd5 SubName: Fu
37	1524	52.6	574	2	Q7Q285_ANOGA	Q7q285 SubName: Fu
38	1493	51.5	574	2	Q17MG1_AEDAE	Q17mg1 SubName: Fu
39	1483.5	51.2	573	2	B0WJR0_CULQU	B0wjrr0 SubName: Fu
40	1469	50.7	593	2	A6RJR5_BOTFB	A6rjr5 SubName: Fu
41	1468.5	50.7	593	2	C5P291_COCP7	C5p291 SubName: Fu
42	1454.5	50.2	593	2	C4JP37_UNCRE	C4jp37 SubName: Fu
43	1449.5	50.0	549	2	B4HJY0_DROSE	B4hjy0 SubName: Fu
44	1443.5	49.8	593	2	C1GG11_PARBD	C1gg11 SubName: Fu
45	1441.5	49.7	553	2	A9UQW8_MONBE	A9uqw8 SubName: Fu

## ALIGNMENTS

## RESULT 1

## VPS45\_HUMAN

ID VPS45\_HUMAN Reviewed; 570 AA.  
AC Q9NRW7; Q15715; Q5T4P6; Q9Y4Z6;  
DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-2000, sequence version 1.  
DT 02-NOV-2010, entry version 81.  
DE RecName: Full=Vacuolar protein sorting-associated protein 45;  
DE Short=h-VPS45;  
DE Short=hlVps45;  
GN Name=VPS45; Synonyms=VPS45A, VPS45B;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=97149272; PubMed=8996080; DOI=10.1016/S0378-1119(96)00367-8;  
RA Pevsner J., Hsu S.-C., Hyde P.S., Scheller R.H.;  
RT "Mammalian homologues of yeast vacuolar protein sorting (vps) genes  
RT implicated in Golgi-to-lysosome trafficking.";  
RL Gene 183:7-14(1996).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Leukocyte;  
RX MEDLINE=99332720; PubMed=10404641; DOI=10.1016/S1357-2725(99)00017-5;  
RA Rajasekariah P., Eyre H.J., Stanley K.K., Walls R.S., Sutherland G.R.;  
RT "Molecular cloning and characterization of a cDNA encoding the human  
RT leucocyte vacuolar protein sorting (hlVps45).";  
RL Int. J. Biochem. Cell Biol. 31:683-694(1999).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Hematopoietic stem cell;  
RA Gu J., Huang Q., Yu Y., Xu S., Han Z., Fu G., Zhou J., Wang Y.,  
RA Huang C., Ren S., Tu Y., Chen Z.;  
RT "Novel genes expressed in hematopoietic stem/progenitor cells from



RT myelodysplastic syndrome patients.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RX PubMed=14702039; DOI=10.1038/ngl285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Sudo H., Hosiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,

RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isoigai T., Sugano S.;

RT "Complete sequencing and characterization of 21,243 full-length human

RT cDNAs.";

RL Nat. Genet. 36:40-45 (2004).

RN [5]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=16710414; DOI=10.1038/nature04727;

RA Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D.,

RA Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A.,

RA Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F.,

RA McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C.,

RA Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P.,

RA Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K.,

RA Babbage A.K., Bagguley C.L., Bailey J., Beasley H., Bethel G.,

RA Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D.,

RA Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G.,

RA Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J.,

RA Deadman R., Dunn M., Earthworm M., Ellington A.G., Errington H.,

RA Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L.,

RA Ghori M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J.,

RA Grafham D.V., Griffiths C., Griffiths-Jones S., Grocock R.,

RA Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D.,

RA Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G.,

RA Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M.,

RA Kershaw J.K., Kibukawa M., Kimberley A.M., King A., Knights A.J.,

RA Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M.,

RA Loveland J., Lovell J., Lush M.J., Lyne R., Martin S.,

RA Mashreghi-Mohammadi M., Matthews L., Matthews N.S.W., McLaren S.,

RA Milne S., Mistry S., Moore M.J.F., Nickerson T., O'Dell C.N.,

RA Oliver K., Palmieri A., Palmer S.A., Parker A., Patel D., Pearce A.V.,

RA Peck A.I., Pelan S., Phelps K., Phillimore B.J., Plumb R., Rajan J.,

RA Raymond C., Rouse G., Saenphimachak C., Sehra H.K., Sheridan E.,

RA Showkneen R., Sims S., Skuce C.D., Smith M., Steward C.,

RA Subramanian S., Sycamore N., Tracey A., Tromans A., Van Helmond Z.,

RA Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E.,

RA Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A.,

RA Vaudin M., Sulston J.E., Durbin R.M., Hubbard T., Wooster R.,

RA Dunham I., Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V.,

RA Beck S., Rogers J., Bentley D.R.;  
 RT "The DNA sequence and biological annotation of human chromosome 1.";  
 RL Nature 441:315-321(2006).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RA Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L.,  
 RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,  
 RA Flanagan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,  
 RA Hannonhalli S., Turner R., Yooshep S., Lu F., Nusskern D.R.,  
 RA Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,  
 RA Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,  
 RA Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,  
 RA Venter J.C.;  
 RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Colon, and Hippocampus;  
 RX PubMed=15489334; DOI=10.1101/gr.2596504;  
 RG The MGC Project Team;  
 RT "The status, quality, and expansion of the NIH full-length cDNA  
 RT project: the Mammalian Gene Collection (MGC).";  
 RL Genome Res. 14:2121-2127(2004).  
 RN [8]  
 RP INTERACTION WITH ZFYVE20.  
 RX MEDLINE=20517446; PubMed=11062261; DOI=10.1083/jcb.151.3.601;  
 RA Nielsen E., Christoforidis S., Uttenweiler-Joseph S., Miaczynska M.,  
 RA Dewitte F., Wilm M., Hoflack B., Zerial M.;  
 RT "Rabenosyn-5, a novel Rab5 effector, is complexed with hVPS45 and  
 RT recruited to endosomes through a FYVE finger domain.";  
 RL J. Cell Biol. 151:601-612(2000).  
 RN [9]  
 RP INTERACTION WITH ZFYVE20.  
 RX PubMed=11788822; DOI=10.1038/ncb744;  
 RA de Renzis S., Soennichsen B., Zerial M.;  
 RT "Divalent Rab effectors regulate the sub-compartmental organization  
 RT and sorting of early endosomes.";  
 RL Nat. Cell Biol. 4:124-133(2002).  
 RN [10]  
 RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RA Colinge J., Superti-Furga G., Bennett K.L.;  
 RL Submitted (OCT-2008) to UniProtKB.  
 CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking  
 CC from the Golgi stack through the trans-Golgi network.  
 CC -!- SUBUNIT: Interacts with STX6 (By similarity). Interacts with  
 CC ZFYVE20.  
 CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral  
 CC membrane protein (By similarity). Endosome membrane; Peripheral  
 CC membrane protein (By similarity). Note=Associated with  
 CC Golgi/endosomal vesicles and the trans-Golgi network (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous. Expression was highest in testis,  
 CC heart and brain, intermediate in kidney, spleen, prostate, ovary,  
 CC small intestine and thymus and low in lung, skeletal muscle,  
 CC placenta, colon, pancreas, peripheral blood leukocytes and liver.  
 CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 -----  
 DR EMBL: U35246; AAC50931.1; -; mRNA.  
 DR EMBL: AJ133421; CAB40417.1; -; mRNA.  
 DR EMBL: AF165513; AAF86643.1; -; mRNA.  
 DR EMBL: AK023170; BAB14443.1; -; mRNA.  
 DR EMBL: AL358073; CAIL4265.1; -; Genomic DNA.  
 DR EMBL: CH471121; EAW53584.1; -; Genomic DNA.  
 DR EMBL: BC012932; AAH12932.1; -; mRNA.  
 DR EMBL: BC028382; AAH28382.1; -; mRNA.  
 DR IPI: IPI00090327; -.  
 DR PIR: JC5722; JC5722.  
 DR RefSeq: NP\_009190.2; -.

DR UniGene; Hs.443750; -.  
 DR ProteinModelPortal; Q9NRW7; -.  
 DR SMR; Q9NRW7; 6-548.  
 DR STRING; Q9NRW7; -.  
 DR PRIDE; Q9NRW7; -.  
 DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.  
 DR GeneID; 11311; -.  
 DR KEGG; hsa:11311; -.  
 DR UCSC; uc001etp.1; human.  
 DR CTD; 11311; -.  
 DR GeneCards; GC01P150039; -.  
 DR H-InvDB; HIX0199801; -.  
 DR HGNC; HGNC:14579; VPS45.  
 DR HPA; HPA027425; -.  
 DR HPA; HPA027441; -.  
 DR MIM; 610035; gene.  
 DR PharmGKB; PA37901; -.  
 DR HOGENOM; HBG559243; -.  
 DR HOVERGEN; HBG059810; -.  
 DR InParanoid; Q9NRW7; -.  
 DR OMA; GTTIHNT; -.  
 DR OrthoDB; EOG9PCDBM; -.  
 DR PhylomeDB; Q9NRW7; -.  
 DR NextBio; 42971; -.  
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Query Match 100.0%; Score 2898; DB 1; Length 570;  
 Best Local Similarity 100.0%;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKS LAEAEQEVEVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKS LAEAEQEVEVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVQKVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLAECVQKVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPOFKKMSGTVSKHVTVVGLESRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPOFKKMSGTVSKHVTVVGLESRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPF LHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPF LHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPDIIIVFVIGGATYEEALTVYNLRNTPGVRIVLG GTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPDIIIVFVIGGATYEEALTVYNLRNTPGVRIVLG GTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 2  
D3DUZ9\_HUMAN  
ID D3DUZ9\_HUMAN Unreviewed; 570 AA.  
AC D3DUZ9;  
DT 23-MAR-2010, integrated into UniProtKB/TreMBL.  
DT 23-MAR-2010, sequence version 1.  
DT 02-NOV-2010, entry version 8.  
DE SubName: Full=Vacuolar protein sorting 45A (Yeast), isoform CRA\_a;  
GN Name=VPS45A; ORFNames=hCG\_39383;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21108353; PubMed=11181995; DOI=10.1126/science.1058040;  
RA Venter J.C., Adams M.D., Myers E.W., Li P.W., Mural R.J., Sutton G.G.,  
RA Smith H.O., Yandell M., Evans C.A., Holt R.A., Gocayne J.D.,  
RA Amanatides P., Ballew R.M., Hsion D.H., Wortman J.R., Zhang Q.,  
RA Kodira C.D., Zheng X.H., Chen L., Skupski M., Subramanian G.,  
RA Thomas P.D., Zhang J., Gabor Miklos G.L., Nelson C., Broder S.,  
RA Clark A.G., Nadeau J., McKusick V.A., Zinder N., Levine A.J.,  
RA Roberts R.J., Simon M., Slayman C., Hunkapiller M., Bolanos R.,  
RA Delcher A., Dew I., Fasulo D., Flanigan M., Florea L., Halpern A.,  
RA Hannenhalli S., Kravitz S., Levy S., Mobarry C., Reinert K.,  
RA Remington K., Abu-Threideh J., Beasley E., Biddick K., Bonazzi V.,  
RA Brandon R., Cargill M., Chandramouliswaran I., Charlab R.,  
RA Chaturvedi K., Deng Z., Di Francesco V., Dunn P., Eilbeck K.,  
RA Evangelista C., Gabriellian A.E., Gan W., Ge W., Gong F., Gu Z.,  
RA Guan P., Heiman T.J., Higgins M.E., Ji R.R., Ke Z., Ketchum K.A.,  
RA Lai Z., Lei Y., Li Z., Li J., Liang Y., Lin X., Lu F., Merkulov G.V.,  
RA Milshina N., Moore H.M., Naik A.K., Narayan V.A., Neelam B.,  
RA Nuskern D., Rusch D.B., Salzberg S., Shao W., Shue B., Sun J.,  
RA Wang Z., Wang A., Wang X., Wang J., Wei M., Wides R., Xiao C., Yan C.,  
RA Yao A., Ye J., Zhan M., Zhang W., Zhang H., Zhao Q., Zheng L.,  
RA Zhong F., Zhong W., Zhu S., Zhao S., Gilbert D., Baumhueter S.,  
RA Spier G., Carter C., Cravchik A., Woodage T., Ali F., An H., Awe A.,  
RA Baldwin D., Baden H., Barnstead M., Barrow I., Beeson K., Busan D.,  
RA Carver A., Center A., Cheng M.L., Curry L., Danaher S., Davenport L.,  
RA Desilets R., Dietz S., Dodson K., Doup L., Ferriera S., Garg N.,  
RA Gluecksmann A., Hart B., Haynes J., Haynes C., Heiner C., Hladun S.,  
RA Hostin D., Houck J., Howland T., Ibegwam C., Johnson J., Kalush F.,  
RA Kline L., Koduru S., Love A., Mann F., May D., McCawley S.,  
RA McIntosh T., McMullen I., Moy M., Moy L., Murphy B., Nelson K.,  
RA Pfannkuch C., Pratts E., Puri V., Qureshi R., Reardon M.,  
RA Rodriguez R., Rogers Y.H., Romblad D., Ruhfel B., Scott R., Sitter C.,  
RA Smallwood M., Stewart E., Strong R., Suh E., Thomas R., Tint N.N.,  
RA Tse S., Vech C., Wang G., Wetter J., Williams S., Williams M.,  
RA Windsor S., Winn-Deen E., Wolfe K., Zaveri J., Zaveri K., Abril J.F.,  
RA Guigo R., Campbell M.J., Sjolander K.V., Karlak B., Kejariwal A.,  
RA Mi H., Lazareva B., Hatton T., Narechania A., Diemer K.,  
RA Muruganujan A., Guo N., Sato S., Bafna V., Istrail S., Lippert R.,  
RA Schwartz R., Walenz B., Yooseph S., Allen D., Basu A., Bendakale J.,  
RA Blick L., Caminha M., Carnes-Stine J., Caulk P., Chiang Y.H.,  
RA Coyne M., Dahlke C., Mays A., Dombroski M., Donnelly M., Ely D.,  
RA Eparham S., Fosler C., Gire H., Glanowski S., Glasser K., Glodek A.,  
RA Gorokhov M., Graham K., Gropman B., Harris M., Heil J., Henderson S.,  
RA Hoover J., Jennings D., Jordan C., Jordan J., Kasha J., Kagan L.,  
RA Kraft C., Levitsky A., Lewis M., Liu X., Lopez J., Ma D., Majoros W.,  
RA McDaniel J., Murphy S., Newman M., Nguyen T., Nguyen N., Modell M.,  
RA Pan S., Peck J., Peterson M., Rowe W., Sanders R., Scott J.,  
RA Simpson M., Smith T., Sprague A., Stockwell T., Turner R., Venter E.,  
RA Wang M., Wen M., Wu D., Wu M., Xia A., Zandieh A., Zhu X.;  
RT "The sequence of the human genome."  
RL Science 291:1304-1351(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Mural R.J., Istrail S., Sutton G., Florea L., Halpern A.L.,  
RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,

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RA Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,
RA Hannehalli S., Turner R., Yooseph S., Lu F., Nusskern D.R.,
RA Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,
RA Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,
RA Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,
RA Venter J.C.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; CH471121; EAW53585.1; -; Genomic_DNA.
DR IPI; IPI00090327; -.
DR RefSeq; NP_009190.2; -.
DR UniGene; Hs.443750; -.
DR ProteinModelPortal; D3DUZ9; -.
DR SMR; D3DUZ9; 2-129.
DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.
DR GeneID; 11311; -.
DR KEGG; hsa:11311; -.
DR CTD; 11311; -.
DR HGNC; HGNC:14579; VPS45.
DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
DR InterPro; IPR001619; Sec1-like.
DR PANTHER; PTHR11679; Sec1-like; 1.
DR Pfam; PF00995; Sec1; 1.
DR SUPFAM; SSF56815; Sec1-like; 1.
PE 4: Predicted;
SQ SEQUENCE 570 AA; 65077 MW; 5574F0BE3A7D4EB3 CRC64;

Query Match 100.0%; Score 2898; DB 2; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTIGVSMVYTQSEILQKEVYLFERIDSQNR 60
Db 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTIGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIIFYFISNVISKSDVKSLAEADEQEVA 120
Db 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIIFYFISNVISKSDVKSLAEADEQEVA 120

Qy 121 EVQEFYGDYIAVNPFLSLNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db 121 EVQEFYGDYIAVNPFLSLNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180

Qy 181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db 181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy 241 GINNMRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFIAEIGSNIKHLMEDFQKKKPK 300
Db 241 GINNMRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFIAEIGSNIKHLMEDFQKKKPK 300

Qy 301 EQQKLESIA DMKAFVENYPOFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Db 301 EQQKLESIA DMKAFVENYPOFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy 361 NDHSSALQNIKRLLNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420
Db 361 NDHSSALQNIKRLLNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420

Qy 421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG 480
Db 421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG 480

Qy 481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRITPGVRIVLGGTIVHNT 540
Db 481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRITPGVRIVLGGTIVHNT 540

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Qy 541 KSFLEEVLAGSLHSRSKESSQVTSRSASRR 570  
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 Db 541 KSFLEEVLAGSLHSRSKESSQVTSRSASRR 570

RESULT 3

Q53FR8\_HUMAN

ID Q53FR8\_HUMAN Unreviewed; 570 AA.  
 AC Q53FR8;  
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 05-OCT-2010, entry version 30.  
 DE SubName: Full=Vacuolar protein sorting 45A variant;  
 DE Flags: Fragment;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Stomach mucosa;  
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;  
 RA Maruyama K., Sugano S.;  
 RT "Oligo-capping: a simple method to replace the cap structure of  
 RT eukaryotic mRNAs with oligoribonucleotides."  
 RL Gene 138:171-174(1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Stomach mucosa;  
 RX MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;  
 RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;  
 RT "Construction and characterization of a full length-enriched and a 5'-  
 RT end-enriched cDNA library."  
 RL Gene 200:149-156(1997).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Stomach mucosa;  
 RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,  
 RA Tanaka A., Yokoyama S.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.  
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 CC -----  
 DR EMBL; AK223214; BAD96934.1; -; mRNA.  
 DR IPI; IPI00090327; -.  
 DR UniGene; Hs.443750; -.  
 DR STRING; Q53FR8; -.  
 DR PhosphoSite; Q53FR8; -.  
 DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.  
 DR HGNC; HGNC:14579; VPS45.  
 DR HOVERGEN; HBG059810; -.  
 DR ArrayExpress; Q53FR8; -.  
 DR Bgee; Q53FR8; -.  
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.  
 DR InterPro; IPR001619; Sec1-like.  
 DR PANTHER; PTHR11679; Sec1-like; 1.  
 DR Pfam; PF00995; Sec1; 1.  
 DR SUPFAM; SSF56815; Sec1-like; 1.  
 FE 2: Evidence at transcript level;  
 FT NON\_TER 1 1  
 SQ SEQUENCE 570 AA; 65070 MW; AD7733351ECEB551 CRC64;

Query Match 99.7%; Score 2888; DB 2; Length 570;  
 Best Local Similarity 99.6%;  
 Matches 568; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNVVFAPQVYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSNQR 60  
 ||||||||||||||||||||||||||||||||



RA Lam T.W., Yiu S.M., Liu S., Zhang H., Li D., Huang Y., Wang X.,  
 RA Yang G., Jiang Z., Wang J., Qin N., Li L., Li J., Bolund L.,  
 RA Kristiansen K., Wong G.K., Olson M., Zhang X., Li S., Yang H.,  
 RA Wang J., Wang J.;  
 RT "The sequence and de novo assembly of the giant panda genome.";  
 RL Nature 463:311-317(2010).  
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 CC -----  
 DR EMBL; GL192667; EFB28489.1; -; Genomic\_DNA.  
 DR RefSeq; XP\_002919362.1; -.  
 DR GeneID; 100471437; -.  
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.  
 DR InterPro; IPR001619; Sec1-like.  
 DR PANTHER; PTHR11679; Sec1-like; 1.  
 DR Pfam; PF00995; Sec1; 1.  
 DR SUPFAM; SSF56815; Sec1-like; 1.  
 PE 4: Predicted;  
 FT NON\_TER 570 570  
 SQ SEQUENCE 570 AA; 65066 MW; F8E11EA1E1372D39 CRC64;

Query Match 99.0%; Score 2868; DB 2; Length 570;  
 Best Local Similarity 98.1%;  
 Matches 559; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTIGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYVSKMIEDSGPGMKVLLMDKETTIGIVSMVYTQSEILQREVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIIFYFSNVISKSDVKS LAEADQE VVA	120
Db	61	EIMKHLKAICFLRPTKENVDYLIQELRRPKYIIFYFSNVISKSDVKS LAEADQE VVA	120
Qy	121	EVQEFYGDYIAVNPPLSLNIGLCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPPLSLNIGLCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVS EKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVS EKYR	420
Qy	421	KLVS AVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTHQPF LHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTHQPF LHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLRITPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLRITPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 5  
 A4FUX9\_BOVIN  
 ID A4FUX9\_BOVIN Unreviewed; 570 AA.



AC A4FUX9;  
 DT 17-APR-2007, integrated into UniProtKB/TrEMBL.  
 DT 17-APR-2007, sequence version 1.  
 DT 05-OCT-2010, entry version 19.  
 DE SubName: Full=VPS45 protein;  
 GN Name=VPS45;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RP STRAIN=L1 Hereford; TISSUE=Thalamus;  
 RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,  
 RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,  
 RA Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,  
 RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,  
 RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,  
 RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;  
 RL Submitted (SEP-2006) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL; BC123422; AAI23423.1; -; mRNA.  
 DR IPI; IPI00718070; -.  
 DR RefSeq; NP\_001076970.1; -.  
 DR UniGene; Bt.13692; -.  
 DR ProteinModelPortal; A4FUX9; -.  
 DR STRING; A4FUX9; -.  
 DR Ensembl; ENSBTAT00000027499; ENSBTAP00000027499; ENSBTAG00000020635.  
 DR GeneID; 541230; -.  
 DR KEGG; bta:541230; -.  
 DR CTD; 541230; -.  
 DR eggNOG; maNOG05713; -.  
 DR HOVERGEN; HBG059810; -.  
 DR InParanoid; A4FUX9; -.  
 DR PhylomeDB; A4FUX9; -.  
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.  
 DR InterPro; IPR001619; Sec1-like.  
 DR PANTHER; PTHR11679; Sec1-like; 1.  
 DR Pfam; PF00995; Sec1; 1.  
 DR SUPFAM; SSF56815; Sec1-like; 1.  
 PE 2: Evidence at transcript level;  
 SQ SEQUENCE 570 AA; 65136 MW; 7D976D91DA92A4F2 CRC64;

Query Match 98.8%; Score 2864; DB 2; Length 570;  
 Best Local Similarity 98.1%;  
 Matches 559; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MNVVFAVQKYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVQKYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYISNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYLIQELRRPKYSIYFYISNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNIIIGCCQGRNWDPAQLSRITQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNIIIGCCQGRNWDPAQLSRITQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVQKVITKEYELFEFRRTVEVPLLLILDRCCDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVQKVITKEYELFEFRRTVEVPLLLILDRCCDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMEDFQKKKPK	300

Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYLALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYLALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Qy	421	KLVSAVVEYGGKRVGSDLFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG	480
Db	421	KLVSAVVEYGGKRVGSDLFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLPGSTLDRPQDIIVFVIGGATYEEALTVYNLRITPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLPGSTLDRPQDIIVFVIGGATYEEALTVYNLRITPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKSSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKSSQVTSRSASRR	570

# RESULT 6

## VPS45\_MOUSE

ID VPS45\_MOUSE Reviewed; 570 AA.

AC P97390; Q91VK9;

DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-MAY-1997, sequence version 1.

DT 05-OCT-2010, entry version 76.

DE RecName: Full=Vacuolar protein sorting-associated protein 45;

DE Short=mVps45;

GN Name=Vps45; Synonyms=Vps45a;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA], AND INTERACTION WITH STX6.

RC STRAIN=Swiss albino; TISSUE=Adipocyte;

RX MEDLINE=97197782; PubMed=9045632; DOI=10.1074/jbc.272.10.6187;

RA Tellam J.T., James D.E., Stevens T.H., Piper R.C.;

RT "Identification of a mammalian Golgi Sec1p-like protein, mVps45.";

RL J. Biol. Chem. 272:6187-6193(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6; TISSUE=Brain, and Mammary tumor;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

RT "The status, quality, and expansion of the NIH full-length cDNA

RT project: the Mammalian Gene Collection (MGC).";

RL Genome Res. 14:2121-2127(2004).

CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking

CC from the Golgi stack through the trans-Golgi network.

CC -!- SUBUNIT: Interacts with ZFYVE20 (By similarity). Interacts with

CC STX6.

CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral

CC membrane protein. Endosome membrane; Peripheral membrane protein.

CC Note=Associated with Golgi/endosomal vesicles and the trans-Golgi

CC network.

CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.

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CC -----

DR EMBL; U66865; AAB37577.1; -; mRNA.

DR EMBL; BC012691; AAH12691.1; -; mRNA.

DR EMBL; BC058528; AAH58528.1; -; mRNA.

DR IPI; IPI00124291; -.

DR RefSeq; NP\_038869.1; -.

DR UniGene; Mm.263185; -.  
 DR ProteinModelPortal; P97390; -.  
 DR SMR; P97390; 6-548.  
 DR STRING; P97390; -.  
 DR PhosphoSite; P97390; -.  
 DR PRIDE; P97390; -.  
 DR Ensembl; ENSMUST00000015891; ENSMUSP00000015891; ENSMUSG00000015747.  
 DR GeneID; 22365; -.  
 DR KEGG; mmu:22365; -.  
 DR UCSC; uc008qly.1; mouse.  
 DR CTD; 22365; -.  
 DR MGI; MGI:891965; Vps45.  
 DR eggNOG; roNOG05944; -.  
 DR HOGENOM; HBG559243; -.  
 DR HOVERGEN; HBG059810; -.  
 DR InParanoid; P97390; -.  
 DR OMA; GTTIHNT; -.  
 DR OrthoDB; EOG9PCDBM; -.  
 DR PhylomeDB; P97390; -.  
 DR NextBio; 302685; -.  
 DR ArrayExpress; P97390; -.  
 DR Bgee; P97390; -.  
 DR CleanEx; MM\_VPS45; -.  
 DR Genevestigator; P97390; -.  
 DR GermOnline; ENSMUSG00000015747; Mus musculus.  
 DR GO; GO:0010008; C:endosome membrane; IDA:MGI.  
 DR GO; GO:0000139; C:Golgi membrane; IDA:MGI.  
 DR GO; GO:0005515; F:protein binding; IPI:MGI.  
 DR GO; GO:0015031; P:protein transport; IEA:UniProtKB-KW.  
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.  
 DR InterPro; IPR001619; Sec1-like.  
 DR PANTHER; PTHR11679; Sec1-like; 1.  
 DR Pfam; PF00995; Sec1; 1.  
 DR SUPFAM; SSF56815; Sec1-like; 1.  
 PE 1: Evidence at protein level;  
 KW Endosome; Golgi apparatus; Membrane; Protein transport; Transport.  
 FT CHAIN 1 570 Vacuolar protein sorting-associated  
 FT protein 45.  
 FT /FTId=PRO\_0000206313.  
 FT CONFLICT 55 55 I -> M (in Ref. 2; AAH12691).  
 SQ SEQUENCE 570 AA; 65053 MW; DA704FDE8469F488 CRC64;

Query Match 98.1%; Score 2844; DB 1; Length 570;  
 Best Local Similarity 97.0%;  
 Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVEYLIQELRRPKSYIYFYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLPSLNIIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLPSLNIIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLGECVKQVISKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLGRVPGISKDLREVVLSAENDEFYANNMYLNFIAEIGSNIKNLMEDFQKKPK	300
Db	241	GINNNRIDLGRVPGISKDLREVVLSAENDEFYANNMYLNFIAEIGSNIKNLMEDFQKKRPK	300
Qy	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360

Qy	361	NDHSSALQNIKRLQLQPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSSEYK 420
Db	361	NDHSSALQNVKRLQLQPKVTEFDAARLVMLYALHYERHSSNSLPLGLIVDLRSKGVAEYK 420
Qy	421	KLVSAYVEYGGKRVGSDLSFSPKDAVAITKQFLKGLKGVENVYVYQHPFLHETLDHLIKG 480
Db	421	KLVSAYVEYGGKRVGSDLSFSPKDAVAITKQFLKGLKGVENVYVYQHPFLHETLDHLIKG 480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRITPGVRIVLGTTVHNT 540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRITPGVRIVLGTTIHNT 540
Qy	541	KSFLEEVLAGSLHRSKSSQVTSRSASRR 570
Db	541	KSFLEEVLAGSLHRSRESSQATRSANRR 570

# RESULT 7

## Q3THX4\_MOUSE

ID Q3THX4\_MOUSE Unreviewed; 570 AA.  
AC Q3THX4;  
DT 11-OCT-2005, integrated into UniProtKB/TreMBL.  
DT 11-OCT-2005, sequence version 1.  
DT 05-OCT-2010, entry version 31.  
DE SubName: Full=Putative uncharacterized protein;  
GN Name=Vps45;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC STRAIN=DBA/2;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilmberg L.G., Aidinis V., Allen J.E.,  
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojorbori T., Green R.E.,  
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Huminick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sadelin A., Schneider C.,  
RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,  
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Bruscia V., Quackenbush J.,  
RA Huestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,



Db 481 RLKENLYPYLGPSTLDRPQDIIVFIIGGATYEEALTVYNLNRITPGVRIVLGGTTIHNT 540

Qy 541 KSFLEEVLAGSLHRSKESQVTSRSASRR 570  
 |||||:|||||:|||| ||||:|

Db 541 KSFLEEVLAGSLHRSRESSQATRSANRR 570

## RESULT 8

## VPS45\_RAT

ID VPS45\_RAT Reviewed; 570 AA.

AC O08700;

DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-JUL-1997, sequence version 1.

DT 05-OCT-2010, entry version 67.

DE RecName: Full=Vacuolar protein sorting-associated protein 45;  
 Short=rVps45;

GN Name=Vps45; Synonyms=Vps45a;  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Brain;

RX MEDLINE=97260358; PubMed=9106478; DOI=10.1016/S0005-2736(97)00014-X;  
 RA El-Husseini A.E.-D., Guthrie H., Snutch T.P., Vincent S.R.;

RT "Molecular cloning of a mammalian homologue of the yeast vesicular  
 transport protein vps45.";

RL Biochim. Biophys. Acta 1325:8-12(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Heart;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

RT "The status, quality, and expansion of the NIH full-length cDNA  
 project: the Mammalian Gene Collection (MGC).";

RL Genome Res. 14:2121-2127(2004).

CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking  
 from the Golgi stack through the trans-Golgi network.

CC -!- SUBUNIT: Interacts with STX6 and ZFYVE20 (By similarity).

CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral  
 membrane protein (By similarity). Endosome membrane; Peripheral  
 membrane protein (By similarity). Note=Associated with  
 Golgi/endosomal vesicles and the trans-Golgi network (By  
 similarity).

CC -!- TISSUE SPECIFICITY: Ubiquitous; expression was highest in testis  
 and in brain. Detected in every part of the brain.

CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.

CC -----

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 CC -----

DR EMBL; U81160; AAB53041.1; -; mRNA.

DR EMBL; BC081705; AAH81705.1; -; mRNA.

DR IPI; IPI00195452; -.

DR RefSeq; NP\_742069.1; -.

DR UniGene; Rn.9316; -.

DR ProteinModelPortal; O08700; -.

DR SMR; O08700; 6-548.

DR MINT; MINT-4576687; -.

DR STRING; O08700; -.

DR PRIDE; O08700; -.

DR Ensembl; ENSRN00000028751; ENSRNOP00000028751; ENSRNOG00000021173.

DR GeneID; 64516; -.

DR KEGG; rno:64516; -.

DR UCSC; NM\_172072; rat.

DR CTD; 64516; -.

DR RGD; 621267; Vps45.

DR eggNOG; roNOG05944; -.

DR HOVERGEN; HBG059810; -.  
 DR InParanoid; O08700; -.  
 DR OMA; GTTHNT; -.  
 DR OrthoDB; EOG9PCDBM; -.  
 DR PhylomeDB; O08700; -.  
 DR NextBio; 613314; -.  
 DR ArrayExpress; O08700; -.  
 DR Genevestigator; O08700; -.  
 DR GermOnline; ENSRNOG00000021173; Rattus norvegicus.  
 DR GO; GO:0010008; C:endosome membrane; IEA:UniProtKB-SubCell.  
 DR GO; GO:0000139; C:Golgi membrane; IEA:UniProtKB-SubCell.  
 DR GO; GO:0015031; P:protein transport; IEA:UniProtKB-KW.  
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.  
 DR InterPro; IPR001619; Sec1-like.  
 DR PANTHER; PTHR11679; Sec1-like; 1.  
 DR Pfam; PF00995; Sec1; 1.  
 DR SUPFAM; SSF56815; Sec1-like; 1.  
 PE 2: Evidence at transcript level;  
 KW Endosome; Golgi apparatus; Membrane; Protein transport; Transport.  
 FT CHAIN 1 570 Vacuolar protein sorting-associated  
 FT protein 45.  
 FT /FTId=PRO\_0000206314.  
 SQ SEQUENCE 570 AA; 64894 MW; 0FF5E2D8E7E7E571 CRC64;

Query Match 98.0%; Score 2840; DB 1; Length 570;  
 Best Local Similarity 97.2%;  
 Matches 554; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEYVLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEYVLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYISNVISKSDVKS LAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDSLIIQELRRPKYTIYFYISNVISKSDVKS LAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLGECVKQVISKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Qy	301	EQQKLESIADMKAFVENYPOFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPOFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSKEYR	420
Db	361	NDHSSALQNVKRLQNPKVTEFDVRLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR	420
Qy	421	KLVS AVVEYGGKRVGSDLFSPKDAVAITKQFLKGLKGVENVYVYTHQPF LHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVGSDLFSPKDAVAITKQFLKGLKGVENVYVYTHQPF LHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSESSQATRSASRR	570

RESULT 9

B7Z360\_HUMAN  
ID B7Z360\_HUMAN Unreviewed; 534 AA.  
AC B7Z360;  
DT 03-MAR-2009, integrated into UniProtKB/TrEMBL.  
DT 03-MAR-2009, sequence version 1.  
DT 05-OCT-2010, entry version 11.  
DE SubName: Full=cDNA FLJ54353, highly similar to Vacuolar protein sorting-associated protein 45;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA TISSUE=Hippocampus;  
RA Wakamatsu A., Yamamoto J., Kimura K., Ishii S., Watanabe K.,  
RA Sugiyama A., Murakawa K., Kaida T., Tsuchiya K., Fukuzumi Y.,  
RA Kumagai A., Oishi Y., Yamamoto S., Ono Y., Komori Y., Yamazaki M.,  
RA Kisu Y., Nishikawa T., Sugano S., Nomura N., Isogai T.;  
RT "NEDO human cDNA sequencing project focused on splicing variants.";  
RL Submitted (OCT-2007) to the EMBL/GenBank/DBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AK295529; BAH12096.1; -; mRNA.  
DR IPI; IPI00090327; -.  
DR UniGene; Hs.443750; -.  
DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.  
DR HGNC; HGNC:14579; VPS45.  
DR HOVERGEN; HBG059810; -.  
DR Bgee; B7Z360; -.  
DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.  
DR InterPro; IPR001619; Sec1-like.  
DR PANTHER; PTHR11679; Sec1-like; 1.  
DR Pfam; PF00995; Sec1; 1.  
DR SUPFAM; SSF56815; Sec1-like; 1.  
DE 2: Evidence at transcript level;  
SQ SEQUENCE 534 AA; 61107 MW; 8FC6896E27D62D59 CRC64;

Query Match	93.7%;	Score 2716;	DB 2;	Length 534;
Best Local Similarity	99.8%;			
Matches 533;	Conservative	1;	Mismatches 0;	Indels 0;
			Gaps 0;	

  

Qy	37	MVYTQSEILQKEVYLFERIDSNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	96
Db	1	MVYTQSEILQKEVYLFERIDSNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	60
Qy	97	YFSNVISKSDVKS LAEADQE VVAEVQEFYGDYIAVNP HFLSLN ILGCCGRNWDPAQLS	156
Db	61	YFSNVISKSDVKS LAEADQE VVAEVQEFYGDYIAVNP HFLSLN ILGCCGRNWDPAQLS	120
Qy	157	RTTQGLTALLSLKKCPMIRYQLSSEA AKRLAECVKQVITKEYELFEFRTEVPPLLLIL	216
Db	121	RTTQGLTALLSLKKCPMIRYQLSSEA AKRLAECVKQVITKEYELFEFRTEVPPLLLIL	180
Qy	217	DRCDDAITPLLNQNTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSEANDEFYANNM	276
Db	181	DRCDDAITPLLNQNTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSEANDEFYANNM	240
Qy	277	YLNFAEIGSINIKNLME DFQKKPKPEQQKLES IADMKAFVENV P QFKKMSGTVSKHVTVVG	336
Db	241	YLNFAEIGSINIKNLME DFQKKPKPEQQKLES IADMKAFVENV P QFKKMSGTVSKHVTVVG	300
Qy	337	ELSRVLSE RNLLEVSEVEQELACQNDHSSALQNIKRL LQNP KVFTEF DAARLVMLYALHYE	396
Db	301	ELSRVLSE RNLLEVSEVEQELACQNDHSSALQNIKRL LQNP KVFTEF DAARLVMLYALHYE	360
Qy	397	RHSSNSLPGLMMDLRNKG VSEKYRKLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGL	456



## SQ SEQUENCE 570 AA; 65048 MW; 722B3FEF9BCE6B497 CRC64;

<http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780f9eb65&ItemName=2010...> 1/10/11

## SCORE Search Results Details for Application 09556178

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203\_114247\_us-09-556-178-1.rpr

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 10 Seconds  
(without alignments)  
5484.355 Million cell updates/sec

Title: US-09-556-178-1  
Perfect score: 2898  
Sequence: 1 MNVVFVRQYISNMIEDSP.....GLASRSESSQVTSRSASRR 570

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, #6216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2833	97.8	570	2 JCS722	vacuolar protein s
2	1299	44.8	569	2 T52056	vacuolar protein s
3	1296	44.7	569	2 T00445	vacuolar protein-s
4	1207.5	41.7	547	2 T23967	hypothetical prote
5	1137.5	39.3	558	2 S62458	vacuolar protein s
6	976	33.7	577	2 J48542	VPS45 protein - ye
7	778.5	26.9	722	2 D71607	VPS45-like protein
8	386.5	13.3	593	2 A55931	nu Sac1 protein -
9	382	13.2	648	2 JCS4674	Sly1 protein - rat
10	376.5	13.1	594	2 A57022	hunc1b-2 - rat
11	372.5	12.9	635	2 T06619	hypothetical prote
12	366	12.6	639	2 T41585	stxbp-us-18-secl
13	361	12.5	673	2 S36747	rop protein - frui
14	355	12.2	592	2 I49239	probable acetylco
15	349.5	12.1	666	2 A39610	vesicle transport
16	344.5	11.9	587	2 S33578	SLYL1 protein - yea
17	339	11.7	733	2 C98258	rop protein - frui
18	338.5	11.7	693	2 T41443	protein FSO11.8 (i
19	333.5	11.5	594	2 S39345	syntaxin-binding p
20	332.5	11.5	594	2 A53495	unc-18 protein hom
21	331.5	11.4	707	2 T22127	hypothetical prote
22	325.5	11.2	594	2 S39346	unc-18 protein hom
23	315.5	10.9	562	2 T32961	hypothetical prote
24	297	10.2	627	2 G84558	probable SEC1 fani
25	235	8.1	724	2 S17479	SEC1 protein - yea
26	207.5	7.2	681	2 JCS720	vacuolar protein s
27	197.5	6.8	592	2 T50328	probable vacuolar
28	168	5.8	576	2 S27790	SLP1 protein homol
29	163	5.6	691	2 A34708	vacuolar protein-s
30	162.5	5.6	535	2 T06734	vacuolar protein s
31	159.5	5.5	617	2 JCS721	vacuolar protein s
32	142	4.9	1005	2 A64065	hypothetical prote
33	142	4.9	1837	2 T41023	probable nuclear p
34	135	4.7	662	2 AG2420	hypothetical prote
35	134.5	4.6	1188	2 F64367	pyruvate, water di
36	133	4.6	944	1 S48821	probable membrane
37	132.5	4.6	1169	2 A64055	PL15 homolog - Mat
38	132.5	4.6	3225	2 T52300	glantin - human
39	132.5	4.6	3209	1 A56319	glantin - human
40	132	4.6	554	2 E90601	hypothetical prote
41	132	4.6	864	2 B90395	purine NTPase [inp
42	132	4.6	1330	2 H89467	protein TOSR9.1 (i
43	132	4.6	1679	2 S48385	hypothetical prote
44	131.5	4.5	886	2 H69378	conserved hypothet
45	131	4.5	833	2 H72205	maltose ABC transp

## ALIGNMENTS

RESULT 1

JCS722

vacuolar protein sorting protein 45 - human

C(Species): Homo sapiens (man)

C(Date): 09-Dec-1997 #sequence\_revision: 09-Dec-1997 #text\_change: 09-Jul-2004

C(Accession): JCS722

R(Fewer, J.; Hsu, S.C.; Hyde, P.S.; Scheller, R.H.

Gene 181: 1-14, 1996

A&gt;Title: Mammalian homologues of yeast vacuolar protein sorting (vps) genes implicated in Golgi-to-lysosome trafficking.

A(Reference number): JCS720; MUID: 97149272; PMID: 8996080

A(Accession): JCS722

A&gt;Status: nucleic acid sequence not shown

A(Molecule type): mRNA



# SCORE Search Results Details for Application 09556178 and Search Result 20101203\_114248\_us-09-556-178-1.ra1.

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 57 Seconds  
(without alignments)  
3961.810 Million cell updates/sec

Title: US-09-556-178-1  
Perfect score: 2898  
Sequence: 1 MNVVFVAVKQYISKMIEDSGP.....GLHSRSKESQVTSRSASRR 570

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2170800 seqs, 396181022 residues

Total number of hits satisfying chosen parameters: 2170800

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /ABSS/Data/CRF/ptodata/1/iaa/5\_COMB.pep:\*  
2: /ABSS/Data/CRF/ptodata/1/iaa/6\_COMB.pep:\*  
3: /ABSS/Data/CRF/ptodata/1/iaa/7\_COMB.pep:\*  
4: /ABSS/Data/CRF/ptodata/1/iaa/H\_COMB.pep:\*  
5: /ABSS/Data/CRF/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /ABSS/Data/CRF/ptodata/1/iaa/RE\_COMB.pep:\*  
7: /ABSS/Data/CRF/ptodata/1/iaa/backfiles1.pep:\*  
SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2898	100.0	570	1	US-08-967-364-1	Sequence 1, Appli
2	2898	100.0	570	2	US-09-368-408-1	Sequence 1, Appli
3	2898	100.0	570	3	US-10-511-937-2612	Sequence 2612, Ap
4	2898	100.0	570	3	US-11-443-428A-738990	Sequence 738990,
5	2898	100.0	570	3	US-11-443-428A-738993	Sequence 738993,
6	2898	100.0	570	3	US-11-443-428A-738994	Sequence 738994,
7	2898	100.0	570	3	US-11-443-428A-739003	Sequence 739003,
8	2844	98.1	570	1	US-08-967-364-7	Sequence 7, Appli
9	2844	98.1	570	2	US-09-368-408-7	Sequence 7, Appli
10	2783	96.0	552	3	US-11-443-428A-738991	Sequence 738991,

11	2777	95.8	552	3	US-11-443-428A-738998	Sequence 738998,
12	2769	95.5	612	3	US-11-443-428A-739002	Sequence 739002,
13	2721	93.9	534	3	US-11-443-428A-738992	Sequence 738992,
14	2721	93.9	534	3	US-11-443-428A-739001	Sequence 739001,
15	2550	88.0	526	3	US-11-443-428A-739004	Sequence 739004,
16	1873	64.6	372	3	US-11-443-428A-738999	Sequence 738999,
17	1755	60.6	359	3	US-11-443-428A-738995	Sequence 738995,
18	1273	43.9	567	3	US-11-241-607-62939	Sequence 62939, A
19	976	33.7	577	2	US-09-487-558B-420	Sequence 420, App
20	917	31.6	398	3	US-10-703-032-125739	Sequence 125739,
21	788	27.2	162	3	US-11-443-428A-739006	Sequence 739006,
22	786.5	27.1	329	3	US-09-417-507-33074	Sequence 33074, A
23	757.5	26.1	200	3	US-11-443-428A-738996	Sequence 738996,
24	744	25.7	158	3	US-11-443-428A-739005	Sequence 739005,
25	613	21.2	129	3	US-11-443-428A-739000	Sequence 739000,
26	492	17.0	230	3	US-10-767-701-43244	Sequence 43244, A
27	416	14.4	212	3	US-09-417-507-33075	Sequence 33075, A
28	386.5	13.3	593	1	US-08-900-927-3	Sequence 3, Appli
29	386.5	13.3	593	1	US-09-191-279-3	Sequence 3, Appli
30	386.5	13.3	593	2	US-09-334-476-3	Sequence 3, Appli
31	384	13.3	95	3	US-11-443-428A-738997	Sequence 738997,
32	383	13.2	628	3	US-11-443-428A-893746	Sequence 893746,
33	383	13.2	633	3	US-11-443-428A-893756	Sequence 893756,
34	382.5	13.2	593	1	US-08-900-927-1	Sequence 1, Appli
35	382.5	13.2	593	1	US-09-191-279-1	Sequence 1, Appli
36	382.5	13.2	593	2	US-09-334-476-1	Sequence 1, Appli
37	382.5	13.2	593	3	US-11-483-373B-2	Sequence 2, Appli
38	382.5	13.2	609	3	US-11-443-428A-857469	Sequence 857469,
39	380.5	13.1	632	3	US-11-443-428A-893751	Sequence 893751,
40	380	13.1	617	3	US-11-443-428A-893748	Sequence 893748,
41	380	13.1	648	3	US-11-443-428A-893749	Sequence 893749,
42	380	13.1	651	3	US-11-443-428A-893754	Sequence 893754,
43	380	13.1	651	3	US-11-443-428A-893758	Sequence 893758,
44	378	13.0	644	3	US-11-443-428A-857458	Sequence 857458,
45	372	12.8	619	3	US-11-443-428A-857474	Sequence 857474,

## ALIGNMENTS

RESULT 1  
US-08-967-364-1  
; Sequence 1, Application US/08967364  
; Patent No. 5989859  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Lal, Preeti  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/967,364  
; FILING DATE: No. 598985September 7, 1997

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIEB01
; CLONE: 75871
US-08-967-364-1

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Query Match 100.0%; Score 2898; DB 1; Length 570;

Best Local Similarity 100.0%;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPF L HETL D H L I K G	480
Db	421	KLVS AVVEYGGKRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPF L HETL D H L I K G	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKSSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKSSQVTSRSASRR	570

RESULT 2

```

US-09-368-408-1
; Sequence 1, Application US/09368408
; Patent No. 6071703
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,364
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIEB01
; CLONE: 75871
US-09-368-408-1
    
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Query Match	100.0%;	Score 2898;	DB 2;	Length 570;				
Best Local Similarity	100.0%;							
Matches 570;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTSQEILQKEVYLFERIDSQNR	60					
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTSQEILQKEVYLFERIDSQNR	60					
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120					
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120					
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180					
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180					
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240					
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240					

Qy	241	GINNNRIDLSRVPGISKDLREVVL	SAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVL	SAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGT	VSXHVTVVGELSRVSERNLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGT	VSXHVTVVGELSRVSERNLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARL	VMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARL	VMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Qy	421	KLVSADVVEYGGKRVRGSDLFSPKDA	VAITKQFLKGLKGVENVYTOHQPFLLHETDLHLIK	480
Db	421	KLVSADVVEYGGKRVRGSDLFSPKDA	VAITKQFLKGLKGVENVYTOHQPFLLHETDLHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVF	VIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVF	VIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSESSQVTSRSASRR	570	
Db	541	KSFLEEVLASGLHSRSESSQVTSRSASRR	570	

RESULT 3

US-10-511-937-2612  
; Sequence 2612, Application US/10511937  
; Patent No. 7691569  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2612  
; LENGTH: 570  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2612

Query Match 100.0%; Score 2898; DB 3; Length 570;  
Best Local Similarity 100.0%;  
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETT	GIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETT	GIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIY	SNVISKSDVKSLAEADEQEVVA	120



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Db          61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSALAEAEQEVVA 120
Qy          121 EVQEFYGDYIYAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
          |||
Db          121 EVQEFYGDYIYAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
Qy          181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240
          |||
Db          181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240
Qy          241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMDQFKKKPK 300
          |||
Db          241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMDQFKKKPK 300
Qy          301 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
          |||
Db          301 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Qy          361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGMMDLRNKGVSEKYR 420
          |||
Db          361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPLGMMDLRNKGVSEKYR 420
Qy          421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG 480
          |||
Db          421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG 480
Qy          481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
          |||
Db          481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Qy          541 KSFL EEVLASGLHSRSKESSQVTSRSASRR 570
          |||
Db          541 KSFL EEVLASGLHSRSKESSQVTSRSASRR 570

```

## RESULT 4

US-11-443-428A-738990

; Sequence 738990, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738990

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738990

Query Match 100.0%; Score 2898; DB 3; Length 570;

Best Local Similarity 100.0%;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIIFYFSNVISKSDVKSLAEAEQEVEVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIIFYFSNVISKSDVKSLAEAEQEVEVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPVPLLILDRCDATPLLMQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPVPLLILDRCDATPLLMQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMEDFQKKPKP	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMEDFQKKPKP	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Qy	421	KLVSADVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETDLHLIKG	480
Db	421	KLVSADVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETDLHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

## RESULT 5

US-11-443-428A-738993

; Sequence 738993, Application US/11443428A

; Patent No. 7745391

## ; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hangqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738993

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738993

```

Query Match          100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFISNVISKSDVKSALAEADEQEVVA 120
Db     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFISNVISKSDVKSALAEADEQEVVA 120

Qy    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
Db    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241  GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDEFQKKPKP 300
Db    241  GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDEFQKKPKP 300

Qy    301  EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVSEARNLLEVSEVEQELACQ 360
Db    301  EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVSEARNLLEVSEVEQELACQ 360

Qy    361  NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLDLRKNKGVSEKYR 420
Db    361  NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLDLRKNKGVSEKYR 420

Qy    421  KLVSAVVEYGGKRRVGSDFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG 480
Db    421  KLVSAVVEYGGKRRVGSDFSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIKG 480

Qy    481  RLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Db    481  RLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541  KSFL EEVLASGLHSRSKESSQVTSRSASRR 570
Db    541  KSFL EEVLASGLHSRSKESSQVTSRSASRR 570

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## RESULT 6

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US-11-443-428A-738994
; Sequence 738994, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443, 428A
; CURRENT FILING DATE: 2006-05-31

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; NUMBER OF SEQ ID NOS: 1034312  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 738994  
 ; LENGTH: 570  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-443-428A-738994

Query Match 100.0%; Score 2898; DB 3; Length 570;  
 Best Local Similarity 100.0%;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKSLAEADEQEVVA 120
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL 240
Db    181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL 240

Qy    241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMDFQKKPKP 300
Db    241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMDFQKKPKP 300

Qy    301 EQQKLESIAIDMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360
Db    301 EQQKLESIAIDMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420
Db    361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420

Qy    421 KLVSAVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG 480
Db    421 KLVSAVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG 480

Qy    481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Db    481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541 KSFLIEVLASGLHSRSKSSQVTSRSASRR 570
Db    541 KSFLIEVLASGLHSRSKSSQVTSRSASRR 570

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## RESULT 7

US-11-443-428A-739003  
 ; Sequence 739003, Application US/11443428A  
 ; Patent No. 7745391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mintz, Liat  
 ; APPLICANT: Xie, Hangqing  
 ; APPLICANT: Dahari, Dvir  
 ; APPLICANT: Levanon, Erez  
 ; APPLICANT: Freilich, Shiri  
 ; APPLICANT: Beck, Nili  
 ; APPLICANT: Zhu, Wei-Yong  
 ; APPLICANT: Wasserman, Alon  
 ; APPLICANT: Hermesh, Chen

```
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 739003
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-739003
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Query Match          100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYQSEILQKEVYLFERIDSQNR 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGDYIAVNPFLFSLNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EVQEFYGDYIAVNPFLFSLNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKKPK 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKKPK 300

Qy    301 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR 420

Qy    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG 480

Qy    481 RLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTIVYNLNRTPGVRIVLGGTTVHNT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 RLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTIVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
      ||||||||||||||||||||||||||||
Db    541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
```

```
RESULT 8
US-08-967-364-7
; Sequence 7, Application US/08967364
; Patent No. 5989859
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
```

```

; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,364
; FILING DATE: No. 5989859ember 7, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI7703494
US-08-967-364-7
    
```

```

Query Match          98.1%; Score 2844; DB 1; Length 570;
Best Local Similarity 97.0%;
Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;
    
```

```

Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR 60
        |||
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR 60
        |||

Qy      61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFISNVISKSDVKS LAEAEDEQEVVA 120
        |||
Db      61 EIMKHLKAICFLRPTKENVEYIIQELRRPKYSIYFYFISNVISKSDVKS LAEAEDEQEVVA 120
        |||

Qy      121 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
        |||
Db      121 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
        |||

Qy      181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWYQAMVHELL 240
        |||
Db      181 SEAAKRLGECVKQVISKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWYQAMVHELL 240
        |||

Qy      241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP 300
        |||
Db      241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP 300
        |||

Qy      301 EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360
        |||
Db      301 EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360
        |||
    
```



Best Local Similarity 97.0%;							
Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;							
Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRIDSNQR	60				
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRIDSNQR	60				
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEQEVEVA	120				
Db	61	EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYFIYFSNVISKSDVKS LAEAEQEVEVA	120				
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180				
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS	180				
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240				
Db	181	SEAAKRLGECVKQVISKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240				
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEFDQKKRKP	300				
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEFDQKKRKP	300				
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360				
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360				
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420				
Db	361	NDHSSALQNVKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLIVDLRSKGVAEKYR	420				
Qy	421	KLVS AVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIKG	480				
Db	421	KLVS AVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIKG	480				
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540				
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFIIGGATYEEALTVYNLNRTPGVRIVLGGTTIHNT	540				
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570				
Db	541	KSFLEEVLASGLHSRSRESSQATRSANRR	570				

## RESULT 10

US-11-443-428A-738991

; Sequence 738991, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738991



```
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738991
```

```
Query Match          96.0%; Score 2783; DB 3; Length 552;
Best Local Similarity 96.8%;
Matches 552; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRIDSQNR 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRIDSQ-- 58

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEDEQEVVA 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59 -----ENVVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEDEQEVVA 102

Qy    121 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    103 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 162

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWITYQAMVHELL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    163 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWITYQAMVHELL 222

Qy    241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    223 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 282

Qy    301 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    283 EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 342

Qy    361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 402

Qy    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETDLHLIKG 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETDLHLIKG 462

Qy    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 522

Qy    541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 KSFLEEVLASGLHSRSKESSQVTSRSASRR 552
```

## RESULT 11

US-11-443-428A-738998

; Sequence 738998, Application US/11443428A

; Patent No. 7745391

## ; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

```

; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738998
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738998

```

```

Query Match          95.8%; Score 2777; DB 3; Length 552;
Best Local Similarity 99.3%;
Matches 547; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

```

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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
      |||
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy      61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYISNVISKSDVKS LAEAEQEVVA 120
      |||
Db      61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYISNVISKSDVKS LAEAEQEVVA 120

Qy      121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
      |||
Db      121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180

Qy      181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDATITPLLNQWTYQAMVHELL 240
      |||
Db      181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDATITPLLNQWTYQAMVHELL 240

Qy      241 GINNRRIDLRSVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKPKP 300
      |||
Db      241 GINNRRIDLRSVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKPKP 300

Qy      301 EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360
      |||
Db      301 EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360

Qy      361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
      |||
Db      361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420

Qy      421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
      |||
Db      421 KLVSAVVEYGGKRVKRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480

Qy      481 RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
      |||
Db      481 RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy      541 KS--FLEEVL A 549
      || || ||
Db      541 KSKRFLREGLA 551

```

```

RESULT 12
US-11-443-428A-739002
; Sequence 739002, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili

```



```

; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738992
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738992

```

```

Query Match          93.9%; Score 2721; DB 3; Length 534;
Best Local Similarity 100.0%;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      37  MVYTSQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI 96
Db      1  MVYTSQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI 60

Qy      97  YFSNVISKSDVKSLAEAEQEVVAEVQEFYGDYIAVNPHLFSLNILGCCQGRNWDPAQLS 156
Db      61  YFSNVISKSDVKSLAEAEQEVVAEVQEFYGDYIAVNPHLFSLNILGCCQGRNWDPAQLS 120

Qy     157  RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTVEPPLLLIL 216
Db     121  RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTVEPPLLLIL 180

Qy     217  DRCDDAITPLLNQWYTYQAMVHELLGINNNRIDLRSVPGISKDLREVVLSAENDEFYANNM 276
Db     181  DRCDDAITPLLNQWYTYQAMVHELLGINNNRIDLRSVPGISKDLREVVLSAENDEFYANNM 240

Qy     277  YLNFABEIGSNIKNLMEDFQKKPKPEQQKLESIA DMKAFVENYQPFKMSGTVSKHVTVVG 336
Db     241  YLNFABEIGSNIKNLMEDFQKKPKPEQQKLESIA DMKAFVENYQPFKMSGTVSKHVTVVG 300

Qy     337  ELSRLVSEARNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE 396
Db     301  ELSRLVSEARNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE 360

Qy     397  RHSSNSLPLGLMDLRNKGVSEKYRKLVS AVVEYGGKRVSGDLFSPKDAVAITKQFLKGL 456
Db     361  RHSSNSLPLGLMDLRNKGVSEKYRKLVS AVVEYGGKRVSGDLFSPKDAVAITKQFLKGL 420

Qy     457  KGVENVYTOHQPFLLHETLDHLIKGRLENLYPYLGPSTLRDRPQDIIVFVIGATYEEAL 516
Db     421  KGVENVYTOHQPFLLHETLDHLIKGRLENLYPYLGPSTLRDRPQDIIVFVIGATYEEAL 480

Qy     517  TVYNLNRTPGVRIVLGGTTVHNHTKSFLEEVLASGLHSRSKESQVTSRSASRR 570
Db     481  TVYNLNRTPGVRIVLGGTTVHNHTKSFLEEVLASGLHSRSKESQVTSRSASRR 534

```

```

RESULT 14
US-11-443-428A-739001
; Sequence 739001, Application US/11443428A

```

```

; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hangqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 739001
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-739001

```

```

Query Match          93.9%; Score 2721; DB 3; Length 534;
Best Local Similarity 100.0%;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy	37	MVYTQSEILQKEVYLFERIDSNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	96
Db	1	MVYTQSEILQKEVYLFERIDSNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	60
Qy	97	YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPHLFSLNILGCCQGRNWDPQLS	156
Db	61	YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPHLFSLNILGCCQGRNWDPQLS	120
Qy	157	RTTQGLTALLLSLKKCPMIRYQLSSEAARKRLAECVKQVITKEYELFEFRRTVEPPLLLIL	216
Db	121	RTTQGLTALLLSLKKCPMIRYQLSSEAARKRLAECVKQVITKEYELFEFRRTVEPPLLLIL	180
Qy	217	DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM	276
Db	181	DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM	240
Qy	277	YLNFAEIGSNIKNLMEDFQKKPKPEQQKLESIA DMKAFVENYQPKKMSGTVSKHVTYVVG	336
Db	241	YLNFAEIGSNIKNLMEDFQKKPKPEQQKLESIA DMKAFVENYQPKKMSGTVSKHVTYVVG	300
Qy	337	ELSRVLSERNLLEVSEVEQELACQNDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYE	396
Db	301	ELSRVLSERNLLEVSEVEQELACQNDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYE	360
Qy	397	RHSSNSLPLGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVSGDLFSPKDAVAITKQFLKGL	456
Db	361	RHSSNSLPLGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVSGDLFSPKDAVAITKQFLKGL	420
Qy	457	KGVENVYTHQHPFLHETLDHLIKGRLENLYPYLGPSTLDRDPQDIIVFVIGGATYEEAL	516
Db	421	KGVENVYTHQHPFLHETLDHLIKGRLENLYPYLGPSTLDRDPQDIIVFVIGGATYEEAL	480
Qy	517	TVYNLNRTPGVRIVLGGTTVHNTKSFLEEVLASGLHSRSKSSQVTSRSASRR	570
Db	481	TVYNLNRTPGVRIVLGGTTVHNTKSFLEEVLASGLHSRSKSSQVTSRSASRR	534

RESULT 15

US-11-443-428A-739004  
 ; Sequence 739004, Application US/11443428A  
 ; Patent No. 7745391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mintz, Liat  
 ; APPLICANT: Xie, Hanqing  
 ; APPLICANT: Dahari, Dvir  
 ; APPLICANT: Levanon, Erez  
 ; APPLICANT: Freilich, Shiri  
 ; APPLICANT: Beck, Nili  
 ; APPLICANT: Zhu, Wei-Yong  
 ; APPLICANT: Wasserman, Alon  
 ; APPLICANT: Hermesh, Chen  
 ; APPLICANT: Azar, Idit  
 ; APPLICANT: Bernstein, Jeanne  
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES  
 ; FILE REFERENCE: 02/23929  
 ; CURRENT APPLICATION NUMBER: US/11/443,428A  
 ; CURRENT FILING DATE: 2006-05-31  
 ; NUMBER OF SEQ ID NOS: 1034312  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 739004  
 ; LENGTH: 526  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-443-428A-739004

Query Match 88.0%; Score 2550; DB 3; Length 526;  
 Best Local Similarity 100.0%;  
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFISNVISKSDVKS LAEAEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFISNVISKSDVKS LAEAEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDP AQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDP AQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNMYLNF AEIGSNIKNLMD EFKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNMYLNF AEIGSNIKNLMD EFKKKPK	300
Qy	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVT VVGELSRVSE RNLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVT VVGELSRVSE RNLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRP	499
Db	481	RLKENLYPYLGPSTLRDRP	499

Search completed: December 3, 2010, 11:43:49  
Job time : 57 secs

SCORE 3 a

# SCORE Search Results Details for Application 09556178 and Search Result 20101203\_114248\_us-09-556-178-1.rapbm.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203\_114248\_us-09-556-178-1.rapbm.

[Go Back to previous page](#)

GenCore version 6.3

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:43:00 ; Search time 201 Seconds  
(without alignments)  
3841.159 Million cell updates/sec

Title: US-09-556-178-1  
Perfect score: 2898  
Sequence: 1 MNVVFVAVKQYISKMIEDSGP.....GLHSRSKESSQVTSRSASRR 570

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6210261 seqs, 1354514112 residues

Total number of hits satisfying chosen parameters: 6210261

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /ABSS/Data/CRF/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /ABSS/Data/CRF/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /ABSS/Data/CRF/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /ABSS/Data/CRF/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /ABSS/Data/CRF/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /ABSS/Data/CRF/ptodata/1/pubpaa/US11A\_PUBCOMB.pep:\*  
7: /ABSS/Data/CRF/ptodata/1/pubpaa/US11B\_PUBCOMB.pep:\*  
8: /ABSS/Data/CRF/ptodata/1/pubpaa/US12\_PUBCOMB.pep:\*

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2898	100.0	570	4	US-10-788-792-187	Sequence 187, App
2	2898	100.0	570	5	US-10-511-937-2612	Sequence 2612, Ap
3	2898	100.0	570	5	US-10-219-051B-7142	Sequence 7142, Ap
4	2898	100.0	570	5	US-10-917-503-15151	Sequence 15151, A
5	2898	100.0	570	6	US-11-371-354-75315	Sequence 75315, A
6	2898	100.0	570	6	US-11-443-428A-738990	Sequence 738990,
7	2898	100.0	570	6	US-11-443-428A-738993	Sequence 738993,
8	2898	100.0	570	6	US-11-443-428A-738994	Sequence 738994,
9	2898	100.0	570	6	US-11-443-428A-739003	Sequence 739003,



10	2898	100.0	570	7	US-11-706-155-684	Sequence 684, App
11	2898	100.0	570	8	US-12-584-615-2612	Sequence 2612, Ap
12	2840	98.0	570	5	US-10-219-051B-7140	Sequence 7140, Ap
13	2815.5	97.2	578	5	US-10-450-763-34837	Sequence 34837, A
14	2783	96.0	552	6	US-11-443-428A-738991	Sequence 738991,
15	2777	95.8	552	6	US-11-443-428A-738998	Sequence 738998,
16	2769	95.5	612	6	US-11-443-428A-739002	Sequence 739002,
17	2721	93.9	534	6	US-11-443-428A-738992	Sequence 738992,
18	2721	93.9	534	6	US-11-443-428A-739001	Sequence 739001,
19	2550	88.0	526	6	US-11-443-428A-739004	Sequence 739004,
20	1873	64.6	372	6	US-11-443-428A-738999	Sequence 738999,
21	1755	60.6	359	6	US-11-443-428A-738995	Sequence 738995,
22	1584	54.7	574	6	US-11-097-143-18048	Sequence 18048, A
23	1310	45.2	441	5	US-10-450-763-34838	Sequence 34838, A
24	1299.5	44.8	567	5	US-10-449-902-43905	Sequence 43905, A
25	1286	44.4	568	4	US-10-437-963-112637	Sequence 112637,
26	1286	44.4	568	5	US-10-437-963-112637	Sequence 112637,
27	1273	43.9	567	6	US-11-241-607-62939	Sequence 62939, A
28	1273	43.9	567	8	US-12-435-281-62939	Sequence 62939, A
29	1270	43.8	567	8	US-12-286-964-7714	Sequence 7714, Ap
30	1089	37.6	567	4	US-10-425-115-238853	Sequence 238853,
31	1089	37.6	567	5	US-10-425-115-238853	Sequence 238853,
32	1030.5	35.6	212	4	US-10-425-115-348394	Sequence 348394,
33	1030.5	35.6	212	5	US-10-425-115-348394	Sequence 348394,
34	976	33.7	577	3	US-09-801-368-420	Sequence 420, App
35	976	33.7	577	3	US-09-800-863-420	Sequence 420, App
36	976	33.7	577	5	US-10-309-407-420	Sequence 420, App
37	917	31.6	398	5	US-10-703-032-125739	Sequence 125739,
38	788	27.2	162	6	US-11-443-428A-739006	Sequence 739006,
39	757.5	26.1	200	6	US-11-443-428A-738996	Sequence 738996,
40	753	26.0	364	5	US-10-449-902-35619	Sequence 35619, A
41	744	25.7	158	6	US-11-443-428A-739005	Sequence 739005,
42	671.5	23.2	303	4	US-10-425-115-238857	Sequence 238857,
43	671.5	23.2	303	5	US-10-425-115-238857	Sequence 238857,
44	613	21.2	129	6	US-11-443-428A-739000	Sequence 739000,
45	574	19.8	219	7	US-11-360-355-123305	Sequence 123305,

## ALIGNMENTS

## RESULT 1

US-10-788-792-187

; Sequence 187, Application US/10788792

; Publication No. US20040191819A1

; GENERAL INFORMATION:

; APPLICANT: Bayer Pharmaceuticals Corporation

; APPLICANT: Eveleigh, Deepa

; APPLICANT: Bigwood, Douglas

; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE

; FILE REFERENCE: 5152

; CURRENT APPLICATION NUMBER: US/10/788,792

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US 60/450,655

; PRIOR FILING DATE: 2003-02-28

; NUMBER OF SEQ ID NOS: 254

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 187

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-788-792-187

Query Match 100.0%; Score 2898; DB 4; Length 570;

Best Local Similarity 100.0%;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVISMVYTQSEILQKEVYLFRERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVISMVYTQSEILQKEVYLFRERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVPPLLLILDRCDDAITPLLMQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVPPLLLILDRCDDAITPLLMQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Qy	421	KLVSADVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETLDHLIKG	480
Db	421	KLVSADVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

## RESULT 2

US-10-511-937-2612

; Sequence 2612, Application US/10511937

; Publication No. US20060088836A1

## ; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511,937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 2612
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2612
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Query Match          100.0%; Score 2898; DB 5; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEQEVEVA 120
Db     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEQEVEVA 120

Qy    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
Db    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241  GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNINKNLMEFDQKKPK 300
Db    241  GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNINKNLMEFDQKKPK 300

Qy    301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSEARNLLEVSEVEQELACQ 360
Db    301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420
Db    361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420

Qy    421  KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPHETLDHLIK 480
Db    421  KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPHETLDHLIK 480

Qy    481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Db    481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541  KSFL EEVLASGLHSRSKESQVTSRSASRR 570
Db    541  KSFL EEVLASGLHSRSKESQVTSRSASRR 570
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# RESULT 3

US-10-219-051B-7142

; Sequence 7142, Application US/10219051B

; Publication No. US20070015145A1

## GENERAL INFORMATION:

; APPLICANT: The General Hospital Corporation doing business as Massachusetts General

; APPLICANT: Hospital / Bayer AG

; TITLE OF INVENTION: Nucleotide sequences involved in pain

; FILE REFERENCE: LeA 35693 Foreign Countries

; CURRENT APPLICATION NUMBER: US/10/219,051B

; CURRENT FILING DATE: 2003-05-09

; PRIOR APPLICATION NUMBER: US 60/312,147

; PRIOR FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: US 60/346,382

; PRIOR FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: US 60/333,347

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; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 7142
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_009189
; DATABASE ENTRY DATE: 2002-11-04
US-10-219-051B-7142

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Query Match          100.0%; Score 2898; DB 5; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
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Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEDEQEVVA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEDEQEVVA 120

Qy    121 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNNRIDL SRVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GINNNRIDL SRVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP 300

Qy    301 EQQKLESIA DMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EQQKLESIA DMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420

Qy    421 KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480

Qy    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541 KSFL EEVLASGLHSRSKESSQVTSRSASRR 570
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Db    541 KSFL EEVLASGLHSRSKESSQVTSRSASRR 570

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RESULT 4
US-10-917-503-15151
; Sequence 15151, Application US/10917503
; Publication No. US20070105122A1
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU

```

```
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15151
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503-15151
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Query Match          100.0%; Score 2898; DB 5; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
Db     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKKCPMIRYQLS 180
Db    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKKCPMIRYQLS 180

Qy    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241  GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK 300
Db    241  GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK 300

Qy    301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Db    301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361  NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR 420
Db    361  NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR 420

Qy    421  KLVSAVVEYGGKRVGRSDFLSPKDAVAITKQFLKGLKGVENVYTHQHPFLHETLDHLIK 480
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Db      421  KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLGKGVENVYTHQPFLLHETLDHLIKG 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      541  KSFLEEVLASGLHSRSKESQVTSRSASRR 570
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  KSFLEEVLASGLHSRSKESQVTSRSASRR 570
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    
```

```

RESULT 5
US-11-371-354-75315
; Sequence 75315, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75315
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-75315
    
```

```

Query Match          100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    
```

```

Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSALAEADEQEVVA 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSALAEADEQEVVA 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      241 GINNRRIDLRSVPGISKDLREVVLSAENDEFYANNMYLFAEIGSNIKNLMDQFKKKPK 300
    
```

```

Db      241  |||||||
GNNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKPKK 300

Qy      301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRVLSERNLLEVSEVEQELACQ 360
|||||

Db      301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRVLSERNLLEVSEVEQELACQ 360

Qy      361  NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR 420
|||||

Db      361  NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR 420

Qy      421  KLVSAVVEYGGKRVSGSDLFSPKDAVAITKQFLKGLKGVENVYVYTHQPFLLHETLDHLIKG 480
|||||

Db      421  KLVSAVVEYGGKRVSGSDLFSPKDAVAITKQFLKGLKGVENVYVYTHQPFLLHETLDHLIKG 480

Qy      481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
|||||

Db      481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy      541  KSFL EEV LASGLHSRSKESQVTSRSASRR 570
|||||

Db      541  KSFL EEV LASGLHSRSKESQVTSRSASRR 570

```

## RESULT 6

US-11-443-428A-738990

; Sequence 738990, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanguing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738990

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738990

Query Match 100.0%; Score 2898; DB 6; Length 570;

Best Local Similarity 100.0%;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
|||||

Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy      61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEAEQEVVA 120
|||||

Db      61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEAEQEVVA 120

Qy      121  EVQEFYGYDIYAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
|||||

Db      121  EVQEFYGYDIYAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

```

```

Qy      181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240
      |||
Db      181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240

Qy      241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK 300
      |||
Db      241 GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMDQFKKKPK 300

Qy      301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSEARNLLEVSEVEQELACQ 360
      |||
Db      301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy      361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR 420
      |||
Db      361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKYR 420

Qy      421 KLVSAVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFPHETLDHLIK 480
      |||
Db      421 KLVSAVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFPHETLDHLIK 480

Qy      481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLRNTPGVRIVLGGTTVHNT 540
      |||
Db      481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLRNTPGVRIVLGGTTVHNT 540

Qy      541 KSFLLEVLAGSLHSRSKESSQVTSRSASRR 570
      |||
Db      541 KSFLLEVLAGSLHSRSKESSQVTSRSASRR 570

```

## RESULT 7

US-11-443-428A-738993

; Sequence 738993, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738993

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738993

Query Match 100.0%; Score 2898; DB 6; Length 570;

Best Local Similarity 100.0%;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
      |||
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy      61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120

```



```

Db      61  |IMFKHLKATCFLRPTKENVVDYIIQELRRPKYTIYFIYFISNIVISKSDVKSIAEAEQEVVA 120
Qy      121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS 180
Db      121  |IMFKHLKATCFLRPTKENVVDYIIQELRRPKYTIYFIYFISNIVISKSDVKSIAEAEQEVVA 180
Qy      181  SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db      181  SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Qy      241  GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKPK 300
Db      241  GINNRRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKPK 300
Qy      301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ 360
Db      301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ 360
Qy      361  NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
Db      361  NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
Qy      421  KLVSAVVEYGGKRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETLDHLIKG 480
Db      421  KLVSAVVEYGGKRVSGDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETLDHLIKG 480
Qy      481  RLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Db      481  RLKENLYPYLGPSTLDRPQDIIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Qy      541  KSFL EEVLASGLHSRSKESSQVTSRSASRR 570
Db      541  KSFL EEVLASGLHSRSKESSQVTSRSASRR 570

```

## RESULT 8

US-11-443-428A-738994

; Sequence 738994, Application US/11443428A

; Publication No. US20070083334A1

## ; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738994

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738994

Query Match 100.0%; Score 2898; DB 6; Length 570;

Best Local Similarity 100.0%;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR  60
      |
Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR  60
      |
Qy     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKS LAEAEDEQEVVA  120
      |
Db     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKS LAEAEDEQEVVA  120
      |
Qy    121  EVQEFYGDYI AVNPHL FSLN ILGCCQGRNWDAQLSRTTQGLTALLSLKKCPMIRYQLS  180
      |
Db    121  EVQEFYGDYI AVNPHL FSLN ILGCCQGRNWDAQLSRTTQGLTALLSLKKCPMIRYQLS  180
      |
Qy    181  SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL  240
      |
Db    181  SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL  240
      |
Qy    241  GINNRRIDL SRVPGISKDLREVVL SAENDEFYANNMYL NFAEIGSNIKNL MEDFQKKPKP  300
      |
Db    241  GINNRRIDL SRVPGISKDLREVVL SAENDEFYANNMYL NFAEIGSNIKNL MEDFQKKPKP  300
      |
Qy    301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVSE RNLLLEVSEVEQELACQ  360
      |
Db    301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTVVGELSRVSE RNLLLEVSEVEQELACQ  360
      |
Qy    361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSL PGLMMDLRNKGVSEKYR  420
      |
Db    361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSL PGLMMDLRNKGVSEKYR  420
      |
Qy    421  KLVSAVVEYGGKRVGRSDLFS PKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG  480
      |
Db    421  KLVSAVVEYGGKRVGRSDLFS PKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG  480
      |
Qy    481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNR TTPGVRIVLGGTTVHNT  540
      |
Db    481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNR TTPGVRIVLGGTTVHNT  540
      |
Qy    541  KSFL EEVLASGLHSRSKESSQVTSRSASRR  570
      |
Db    541  KSFL EEVLASGLHSRSKESSQVTSRSASRR  570

```

## RESULT 9

US-11-443-428A-739003

; Sequence 739003, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 739003

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens  
US-11-443-428A-739003

Query Match 100.0%; Score 2898; DB 6; Length 570;  
Best Local Similarity 100.0%;  
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVISVMYQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVISVMYQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEAEQEVEVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEAEQEVEVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLMQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCCDAITPLLMQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPKP	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMDLRNKGVSEKYR	420
Qy	421	KLVSADVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFPLHETLDHLIKG	480
Db	421	KLVSADVVEYGGKRRVSGDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFPLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

# RESULT 10

US-11-706-155-684

; Sequence 684, Application US/11706155

; Publication No. US20080075722A1

## ; GENERAL INFORMATION

; APPLICANT: DEPINHO, RONALD A.

; APPLICANT: ANDERSON, KENNETH C.

; APPLICANT: CARRASCO, DANIEL R.

; APPLICANT: TONON, GIOVANNI

; APPLICANT: BRENNAN, CAMERON

; APPLICANT: SHAUGHNESSY, JOHN D., Jr.

; APPLICANT: CHIN, LYNDIA

; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,

; TITLE OF INVENTION: PREVENTION, AND THERAPY OF CANCER

; FILE REFERENCE: DFS-065.01

; CURRENT APPLICATION NUMBER: US/11/706,155

; CURRENT FILING DATE: 2007-11-09

; PRIOR APPLICATION NUMBER: 60/773,072

; PRIOR FILING DATE: 2006-02-14

; NUMBER OF SEQ ID NOS: 713  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 684  
 ; LENGTH: 570  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-706-155-684

Query Match 100.0%; Score 2898; DB 7; Length 570;  
 Best Local Similarity 100.0%;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEDEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEDEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMD FQKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMD FQKKPK	300
Qy	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSR LVSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSR LVSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVY TQHPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVY TQHPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSPLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSPLEEVLASGLHSRSKESQVTSRSASRR	570

## RESULT 11

US-12-584-615-2612

; Sequence 2612, Application US/12584615

; Publication No. US20100151467A1

; GENERAL INFORMATION

; APPLICANT: XDx, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

```
; TITLE OF INVENTION:AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000123
; CURRENT APPLICATION NUMBER: US/12/584,615
; CURRENT FILING DATE: 2009-09-23
; PRIOR APPLICATION NUMBER: US 10/511,937
; PRIOR FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: PCT/US2003/12946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 13083
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2612
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-12-584-615-2612
```

```
Query Match          100.0%; Score 2898; DB 8; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEQEVEVA 120
Db     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKS LAEAEQEVEVA 120

Qy    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLK KCPMIRYQLS 180
Db    121  EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLK KCPMIRYQLS 180

Qy    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYTQAMVHELL 240
Db    181  SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYTQAMVHELL 240

Qy    241  GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKPKP 300
Db    241  GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKPKP 300

Qy    301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVVGELSRLVSE RNLLLEVSEVEQELACQ 360
Db    301  EQQKLESIADMKAFVENYYPQFKKMSGTVSKHVTTVVGELSRLVSE RNLLLEVSEVEQELACQ 360

Qy    361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420
Db    361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSEKYR 420

Qy    421  KLVSAVVEYGGKRRVGSDFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIK 480
Db    421  KLVSAVVEYGGKRRVGSDFSPKDAVAITKQFLKGLKGVENVYTHQFPFLHETLDHLIK 480

Qy    481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Db    481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541  KSFL EEVLASGLHSRSKES SQVTSRSASRR 570
Db    541  KSFL EEVLASGLHSRSKES SQVTSRSASRR 570
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```
RESULT 12
US-10-219-051B-7140
```



Db 541 KSPLEEVLASGLHSRSRESSQATRSASRR 570

## RESULT 13

US-10-450-763-34837  
 ; Sequence 34837, Application US/10450763  
 ; Publication No. US20050196754A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 ; FILE REFERENCE: 790CIP3/US  
 ; CURRENT APPLICATION NUMBER: US/10/450,763  
 ; CURRENT FILING DATE: 2003-06-11  
 ; PRIOR APPLICATION NUMBER: PCT/US01/08631  
 ; PRIOR FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: 09/540,217  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR APPLICATION NUMBER: 09/649,167  
 ; PRIOR FILING DATE: 2000-08-23  
 ; NUMBER OF SEQ ID NOS: 60736  
 ; SOFTWARE: Custom  
 ; SEQ ID NO 34837  
 ; LENGTH: 578  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: DOMAIN  
 ; LOCATION: (218)..(258)  
 ; OTHER INFORMATION: Sec1 family domain identified by eMATRIX, accession number  
 ; OTHER INFORMATION: PF00995B, p-value=6.745e-25, raw score of 17.37  
 ; FEATURE:  
 ; NAME/KEY: DOMAIN  
 ; LOCATION: (95)..(562)  
 ; OTHER INFORMATION: Sec1 family domain identified by PFam, accession name Sec1, E  
 ; OTHER INFORMATION: -value=2.9e-164, PFam score of 559.1  
 US-10-450-763-34837

Query Match 97.2%; Score 2815.5; DB 5; Length 578;  
 Best Local Similarity 97.7%;  
 Matches 558; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRERIDSNQR	60
Db	8	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFRERIDSNQR	67
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIIFYFSNVISKSDVKSLA-EADEQEVV	119
Db	68	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIIFYFSNVISKSDVEVIGLKLIEQEVV	127
Qy	120	AEVQEFYGDYIAVNPHLFSLNILGCCQGRNWDPAPQLSRTTQGLTALLSLKKCPMIRYQL	179
Db	128	AEVQEFYGDYIAVNPHLFSLNILGCCQGRNWDPAPQLSRTTQGLTALLSLKKCPMIRYQL	187
Qy	180	SSEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHEL	239
Db	188	SSEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHEL	247
Qy	240	LGINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKP	299
Db	248	LGINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKP	307
Qy	300	KEQQLKLESIGMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELAC	359
Db	308	KEQQLKLESIGMKAFVENYPQFKKMSGTVSKHVTVVGELSRVLSERNLLEVSEVEQELAC	367
Qy	360	QNDHSSALQNIKRLLNQPNKVTEFDAARLVMLYALHYERHSSNSLPLGMLMDLRNKGVSEKY	419

```

Db          368 QNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPLGLMMDLRNKGVSSEY 427
              |||
Qy          420 RKLVSAAVVEYGGKRVGRSGLFSPKDAVAITKQFLKGLKGVENVYQHPFLHETLDHLIK 479
              |||
Db          428 RKLVSAAVVEYGGKRVGRSGLFSPKDAVAITKQFLKGLKGVENVYQHPFLHETLDHLIK 487
              |||
Qy          480 GRLENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHN 539
              |||
Db          488 GRLENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHN 547
              |||
Qy          540 TKSFLAEVLASGLHSRSKSSQVTSRSASRR 570
              |||
Db          548 TKSFLAEVLASGLHSRSKSSQVTSRSASRR 578
              |||

```

## RESULT 14

```

US-11-443-428A-738991
; Sequence 738991, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738991
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738991

```

```

Query Match          96.0%; Score 2783; DB 6; Length 552;
Best Local Similarity 96.8%;
Matches 552; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

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Qy          1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVISMVYQSEILQKEVYLFERIDSQNR 60
              |||
Db          1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVISMVYQSEILQKEVYLFERIDSQ-- 58
              |||
Qy          61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEAEQEVVA 120
              |||
Db          59 -----ENVVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEAEQEVVA 102
              |||
Qy          121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
              |||
Db          103 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 162
              |||
Qy          181 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQYAMVHELL 240
              |||
Db          163 SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQYAMVHELL 222
              |||
Qy          241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKKPK 300
              |||
Db          223 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDEFQKKKPK 282
              |||

```



Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	360
Db	283	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRVLSERNLLEVSEVEQELACQ	342
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	343	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	402
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETLDHLIKG	480
Db	403	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTHQPFPLHETLDHLIKG	462
Qy	481	RLKENLYPYLPGSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	463	RLKENLYPYLPGSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	522
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	523	KSFLEEVLASGLHSRSKESSQVTSRSASRR	552

## RESULT 15

US-11-443-428A-738998

; Sequence 738998, Application US/11443428A

; Publication No. US20070083334A1

## ; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738998

; LENGTH: 552

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738998

Query Match 95.8%; Score 2777; DB 6; Length 552;

Best Local Similarity 99.3%;

Matches 547; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEQEYVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFISNVISKSDVKS LAEAEQEYVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWYQAMVHELL	240

```

Db      181  SEAAKRLAECVKQVITKEYELFEFRRTVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Qy      241  GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKKPK 300
Db      241  GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKKPK 300
Qy      301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Db      301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Qy      361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
Db      361  NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
Qy      421  KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG 480
Db      421  KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG 480
Qy      481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Db      481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
Qy      541  KS--FLEEVLA 549
Db      541  KSKRFLREGLA 551

```

Search completed: December 3, 2010, 11:46:57  
 Job time : 237 secs

SCORE 5.6

# SCORE Search Results Details for Application 09556178 and Search Result 20101203\_114249\_us-09-556-178-1.rapbn.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203\_114249\_us-09-556-178-1.rapbn.

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GenCore version 6.3  
Copyright (c) 1993 - 2010 Biocacceleration Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:55 ; Search time 5 Seconds  
(without alignments)  
160.331 Million cell updates/sec

Title: US-09-556-178-1  
Perfect score: 2898  
Sequence: 1 MNVVFVAVKQYISKMIEDSGP.....GLHSRSKESQVTSRSASRR 570

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 14841 seqs, 1406414 residues

Total number of hits satisfying chosen parameters: 14841

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /ABSS/Data/CRF/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
2: /ABSS/Data/CRF/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
3: /ABSS/Data/CRF/ptodata/1/pubpaa/US12\_NEW\_PUB.pep:\*  
SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	123.5	4.3	980	3 US-12-293-792A-10	Sequence 10, Appl
2	117	4.0	500	3 US-12-441-092-4	Sequence 4, Appli
3	117	4.0	667	3 US-12-441-092-2	Sequence 2, Appli
4	114	3.9	1977	3 US-12-739-689-45	Sequence 45, Appl
5	114	3.9	1977	3 US-12-739-723-39	Sequence 39, Appl
6	113	3.9	1396	3 US-12-086-571-50	Sequence 50, Appl
7	109	3.8	488	3 US-12-086-571-175	Sequence 175, App
8	107.5	3.7	813	3 US-12-739-689-36	Sequence 36, Appl
9	107.5	3.7	2325	3 US-12-739-689-28	Sequence 28, Appl
10	107.5	3.7	2325	3 US-12-739-723-30	Sequence 30, Appl
11	99.5	3.4	2757	3 US-12-625-053A-38	Sequence 38, Appl
12	99	3.4	755	3 US-12-345-877-181	Sequence 181, App
13	97.5	3.4	1960	3 US-12-864-218-90	Sequence 90, Appl
14	96.5	3.3	483	3 US-12-441-092-41	Sequence 41, Appl

15	96.5	3.3	1979	3	US-12-739-689-47	Sequence 47, Appl
16	96.5	3.3	1979	3	US-12-739-723-41	Sequence 41, Appl
17	96	3.3	3692	3	US-12-625-053A-48	Sequence 48, Appl
18	95.5	3.3	1014	3	US-12-345-877-251	Sequence 251, App
19	95	3.3	334	3	US-12-441-092-8	Sequence 8, Appli
20	95	3.3	501	3	US-12-441-092-6	Sequence 6, Appli
21	94	3.2	787	3	US-12-739-689-54	Sequence 54, Appl
22	94	3.2	808	3	US-12-523-023-3	Sequence 3, Appli
23	93.5	3.2	534	3	US-12-764-333A-3	Sequence 3, Appli
24	93.5	3.2	794	3	US-12-523-023-4	Sequence 4, Appli
25	92	3.2	878	3	US-12-733-159A-166	Sequence 166, App
26	91.5	3.2	788	3	US-12-739-689-55	Sequence 55, Appl
27	90.5	3.1	408	3	US-12-441-092-43	Sequence 43, Appl
28	90.5	3.1	872	3	US-12-523-023-1	Sequence 1, Appli
29	88	3.0	303	3	US-12-441-092-40	Sequence 40, Appl
30	88	3.0	332	3	US-12-441-092-39	Sequence 39, Appl
31	88	3.0	2005	3	US-12-317-496-34	Sequence 34, Appl
32	87.5	3.0	913	3	US-12-086-571-250	Sequence 250, App
33	87.5	3.0	1757	3	US-12-787-298-15	Sequence 15, Appl
34	87	3.0	295	3	US-12-625-053A-50	Sequence 50, Appl
35	87	3.0	562	3	US-12-086-571-242	Sequence 242, App
36	87	3.0	2005	3	US-12-317-496-35	Sequence 35, Appl
37	87	3.0	2339	3	US-12-739-689-26	Sequence 26, Appl
38	87	3.0	2339	3	US-12-739-723-26	Sequence 26, Appl
39	87	3.0	2589	3	US-12-739-689-42	Sequence 42, Appl
40	87	3.0	2589	3	US-12-739-723-28	Sequence 28, Appl
41	85.5	3.0	801	3	US-12-784-310-2	Sequence 2, Appli
42	85	2.9	858	3	US-12-682-544-14	Sequence 14, Appl
43	85	2.9	858	3	US-12-682-544-15	Sequence 15, Appl
44	85	2.9	858	3	US-12-682-544-16	Sequence 16, Appl
45	84.5	2.9	530	3	US-12-784-310-17	Sequence 17, Appl

## ALIGNMENTS

## RESULT 1

US-12-293-792A-10

; Sequence 10, Application US/12293792A

; Publication No. US20100297178A1

; GENERAL INFORMATION

; APPLICANT: Murdoch University

; TITLE OF INVENTION: Novel Genes and Proteins of *Brachyspira hyodysenteriae* and Use of

; TITLE OF INVENTION: Same for Diagnosis and Therapy

; FILE REFERENCE: P78788.US

; CURRENT APPLICATION NUMBER: US/12/293,792A

; CURRENT FILING DATE: 2010-07-15

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: PatentIn version 3.5

; SEQ ID NO 10

; LENGTH: 980

; TYPE: PRT

; ORGANISM: *Brachyspira hyodysenteriae*

US-12-293-792A-10

Query Match 4.3%; Score 123.5; DB 3; Length 980;

Best Local Similarity 18.2%;

Matches 124; Conservative 106; Mismatches 262; Indels 191; Gaps 26;

```

Qy      5 FAVKQYISKMIED-----SGPGMKVLLMDKETTIGVSMVYTQSEI----- 44
||:  :  : : |          ||| | : | | | : | : | : | : | : | : | : |
Db      228 FAIVDEVDSILIDEARTPLIISGPAEKNIKMYEIDRIIPML-KQAEVDERMREVAGTGD 286

Qy      45 -----LQKEVYLFER-----IDSQNREIMKHL-KAICFLRPRTKENVDYIIQ 84
          | || |              :| : | : | : | : | : | : | : | : | : |
Db      287 YVLDEKDKNVYLTEEGVHKVEKLLNVENLYGAQSSSTIVHHVNQALKAKHKVFKKDVDMYT 346

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